

REPLACEMENT SHEET

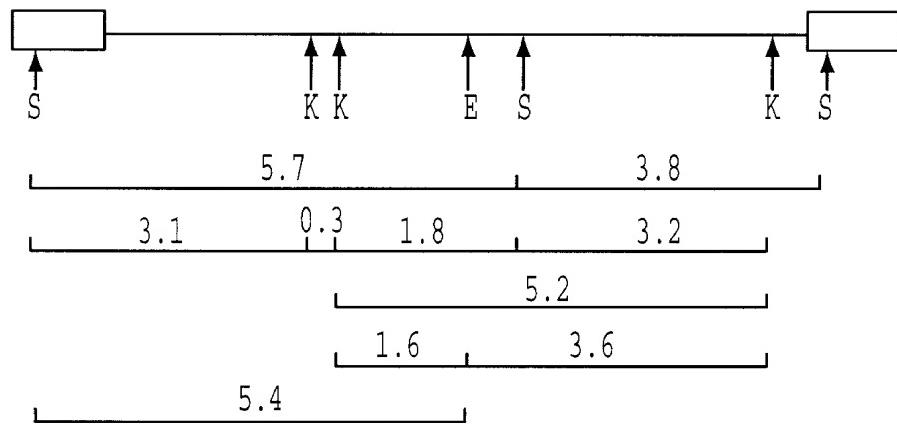


FIG. 1

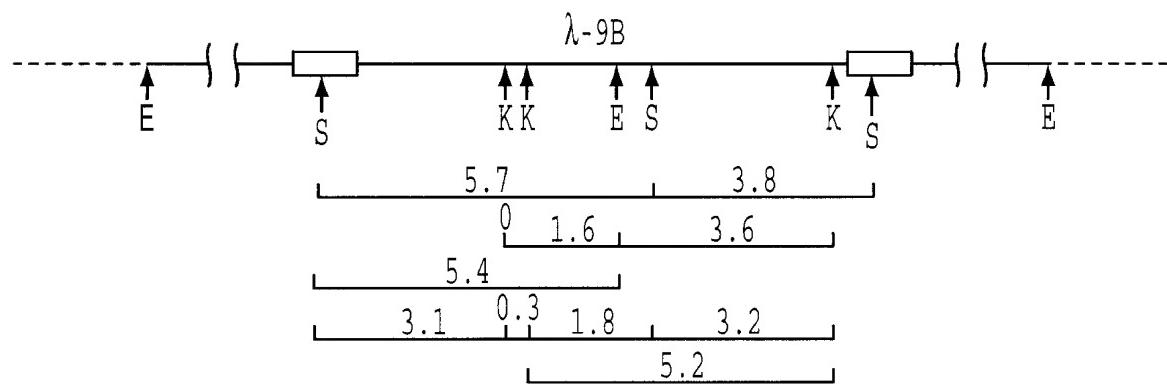


FIG. 2

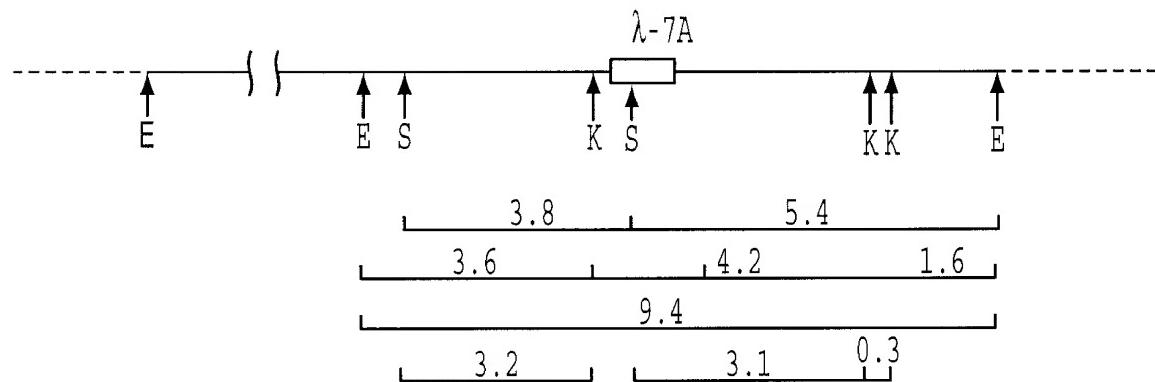


FIG. 3

REPLACEMENT SHEET

Argument Map in DNA Strand ssarv2
 from the '/v/lib/6mers' file.
 Translation shown at open reading frames.

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-!----!-----!----- !!!!-----!!-----!-----!!--
mbol1-1 mbol1-1          bgI11      nar1      xmn1      pst1
binI      binI           aval-2      sac1      sac1
          binI           scal       af111
          ecor5          hind111
                                af111
                                hind111

-----!-----!-----!-----!-----!-----!-----!!--
hind111  ahal11  pst1      bstXI     ahal11  apal
mbol1-1  ava3   ahal11  mbol1-1  sph1   mbol1-1  avr2
          mbol1-1
          pvull
          pst1
          pvull
          tthIIII-2

-----!-----!-----!-----!-----!-----!-----!!--
mbol1-2  mbo11-1  mbo11-1  scal      ava3   tthIIII-2
mbol1-1  mbol1-1  bstXI    ahal11  tthIIII-2
          mbol1-1
          bgl11
          ball
          mbol1-1

-----!-----!-----!-----!-----!-----!-----!!--
binI      bstXI  mbol1-1  ahal11  hpa1      kpnl  mbo11-1
          pvull
          tthIIII-2
          ahal11
          mbol1-1
          ava3

-----!-----!-----!-----!-----!-----!-----!!--
kpnl  mbo11-1  bstXI  mbo11-1  af111  hind111
scal  pvull   xmn1  scal   ahal11  mbol1-1
ava3  ball
xba1  binI

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FIG. 4A

REPLACEMENT SHEET

-!_!!_!-----!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!

ndel avr2 avr2 binI mboll-1 ecorl avr2 mboll-1
scal binI aflll mboll-1 mboll-1
 avr2 xbal sacl
 ncol mlul hindlll
 mstII

-!_!_!-----!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!

scal mboll-1 ndel binI mboll-1 stul mboll-1
mboll-1 ahal11 scal mboll-1
 bglll pvull

-!_!_!-----!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!

mboll-1 mstII mboll-2 mboll-1 mstII
 mstII binI avr2
 mboll-1

!_!

mboll-1 aval-2 pstl mboll-1 aval-1 ahal11
mboll-1 mboll-1 tthlll-2 mboll-1
mboll-1 xhol mstII binI
bglll mboll-1 kpn1
mboll-2

-!_!_!_!_!_!_!_!_!_!_!_!_!_!_!_!

ecor5 aval-2 pvull
mboll-1 bglll
binI scal sacl
 aflll
 hindlll

FIG. 4B

REPLACEMENT SHEET

1 CTGGAAGGGCTAATTGGTCCAAAGAACAGACAAGAGATCCTGATCTGTGGATCTACCACAC
 GACCTTCCGATTAAACCAGGGTTCTTCTGTTCTAGGA~~ACTAGAC~~ACTAGATGGTGTG
 26 mbol1, 50 bin1,

63 ACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACT
 TGTTCGATGAAGGGACTAACCGTCTTAATGTGTGGTCCC~~G~~GTCC~~T~~AGTCTATAGGTGA
 107 bin1, 113 ecor5,

123 GACCTTGATGGTGCTCAAGCTAGTACCA~~G~~AGTTGAGCCAGAGAAGGTAGAAGAGGCCAA
 CTGGAAACCTACCACGAAGTTGATCATGGTCAACTCGGTCTTCCAT~~C~~TTCTCCGGTT
 172 mbol1,

183 TGAAGGAGAGAACAA~~C~~AGCTTACACCCATGAGCCTGCATGGGATGGAGGACGCCGA
 ACTTCC~~T~~CTCTTGTGTCGAACAATGTGGGATACTCGGACGTACCC~~T~~ACCTCC~~T~~GC~~G~~CCT

243 GAAAGAAGT~~T~~AGTGTGGAGGTTGACAGCAA~~A~~CTAGCATT~~C~~ATCACATGGCCCAGA
 CTTCTTCA~~A~~ATCACACCT~~C~~AA~~A~~CTGTGTTGATCGTAAAGTAGTGTACCGGGCTCT
 296 ~~aval~~,

303 GCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTCTACAAGGGACTTCCGC
 CGACGTAGGCC~~T~~CATGATGTTCTGACGACTGTAGCTGAAAGATGTTCC~~T~~GAAAGGCG
 314 ~~scal~~,

363 TGGGGACTTCCAGGGAGGC~~G~~GTGGCCTGGC~~G~~CTGGC~~G~~GGACTGGGAGTGGCGTCC~~T~~CAGATGC
 ACCC~~T~~GAAAGGTCC~~T~~CCG~~C~~ACCGGACCC~~T~~GACCC~~T~~CACCGCAGGGAGTCTACG

423 TGCATATAAGCAGACTGCTTTGCCTGTACTGGGTCTCTGGTTAGACCAGATCTGAG
 ACGTATATT~~C~~GTCTGACGAAAACGGACATGACCCAGAGAGACCA~~A~~TCTGG~~T~~AGACTC
 474 bg111,

483 CCTGGGAGCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAGCTTGCCTT
 GGACCC~~T~~CGAGAGACC~~G~~ATTGATCC~~T~~GGTGAC~~G~~AATT~~C~~GGAGTTATT~~T~~CGAACGGAA
 488 ~~sac1~~, 518 af111, 532 hind111,

543 GAGTGCTTCAAGTAGTGTGCCCC~~G~~TCTGTGTGACTCTGGTA~~A~~CTAGAGATCCCTCA
 CTCACGAAGTT~~C~~ATCACACACGGCAGACAACACACTGAGACCATTGATCTAGGGAGT

603 GACC~~T~~TTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCC~~G~~GAACAGGGACGCCAAAG
 CTGGGAAAATCAGTCACAC~~T~~TTAGAGATCGTCA~~C~~CCGGGGCTTGTCC~~T~~CGC~~T~~TC
 639 ~~nar1~~,

663 CGAAAGTAGAACCA~~G~~AGAGGAGCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACAG
 GCTTCATTTGGTCTCC~~T~~CGAGAGAGCTGCGTCTGAGCCGAACGACTTC~~G~~CGCGT~~G~~T~~C~~
 680 ~~sac1~~,

723 CAAGAGGCAGGGGCGGC~~G~~ACTGGTGAGTACGCCAATTTTGACTAGCGGAGGCTAGAAG
 GTTCTCCGCTCCCCGCGCTGACCACTCATGCGGTTAAA~~A~~ACTGATGCC~~T~~CCGATCTTC

783 GAGAGAGAGATGGGTGCGAGAGCGT~~C~~GGTATTAGC~~G~~GGGGAGAATTAGATAAA~~A~~ATGGGAA
 CTCTCTCTACCCACGCTCTCGCAGCCATAATT~~C~~GCCCCCTTTAATCTATTACCC~~T~~

MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspLysTrpGlu GAG

FIG. 4C

REPLACEMENT SHEET

843 LysIleArgLeuArgProGlyGlyLysLysTyrLysLeuLysHisIleValTrpAla
 AAAATTCCGTTAACGGCAGGGGGAAAGAAAAAATATAAGTTAAAACATATAGTATGGGCA
 TTTAAGCCAATTCCGGTCCCCCTTCTTTTATATTCAATTGTATATCATAACCGT

 903 SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
 AGCAGGGAGCTAGAACGATTCCGAGTCATCCTGGCCTGTTAGAAACATCAGAAGGCTGC
 TCGTCCCTCGATCTTGCTAACGCTAGTTAGGACCGGACAATCTTGTAGTCTTCCGAC
 959 pst1,

 963 ArgGlnIleLeuGlyGlnLeuGlnProSerLeuGlnThrGlySerGluGluLeuArgSer
 AGACAAATATTGGGACAGCTACAGCCATCCCTCAGACAGGATCAGAAGAACTTAGATCA
 TCTGTTATAACCCTGTCATGTCGGTAGGGAAGTCTGTCTAGTCTTGAATCTAGT
 1002 binI, 1008 mboll,

 1023 LeuTyrAsnThrValAlaThrLeuTyrCysValHisGlnArgIleAspValLysAspThr
 TTATATAATACAGTAGCAACCTCTATTGTGTACATCAAAGGATAGATGTAAGAACACC
 AATATATTATGTCATCGTTGGGAGATAACACATGTAGTTCTATCTACATTTCTGTGG

 1083 LysGluAlaLeuGluLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGin
 AAGGAAGCTTAGAGAAGATAGAGGAAGAGCAAAACAAAGTAAGAAAAAGGCACAGCAA
 TTCCCTCGAAATCTCTCTATCTCCTCTCGTTTGTCTTCAATTCTTTCCGTGTCGTT
 1087 hindIII, 1097 mboll, 1107 mboll, p25

 1143 AlaAlaAlaAlaAlaGlyThrGlyAsnSerSerGlnValSerGlnAsnTyrProIleVal
 GCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTCAGCCAAATTACCCCTATAGTG
 CGTCGTCGACGTCGACCGTGTCCCTTGTGTCGGTCCAGTCGGTTTAATGGGATATCAC
 1147 pvuII, 1150 pst1, 1153 pvuII, 1156 tthIII,

 1203 GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
 CAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACCTTAAATGCATGG
 GTCTGGATGTCGGTACCATGTAGTCCGGTATAGTGGATCTGAAATTACGTAC
 1250 ahaIII, 1255 ava3,

 1263 ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
 GTAAAAGTAGTAGAAGAAAAGGCTTCAGCCCAGAAGTAATACCATGTTTCAGCATTA
 CATTTTCATCATCTTCTTTCCGAAAGTCGGTCTTCATTATGGGTACAAAGTCGTAAT
 1275 mboll,

 1323 SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
 TCAGAAGGAGCCACCCCACAAGATTAAACACCATGCTAACACACAGTGGGGGACATCAA
 AGTCTTCTCGGTGGGTGTTCTAAATTGTGGTACGATTGTGTCACCCCTGTAGTT
 1346 ahaIII,

 1383 AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal
 GCAGCCATGAAATGTTAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATAGAGTG
 CGTCGGTACGTTACAATTCTGTAGTTACTCCTCGACGTCTACCCCTATCTCAC
 1423 pst1,

 1443 HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp
 CATCCAGTGCATGCAGGGCTATTGCACCAAGGCCAAATGAGAGAACCAAGGGAAAGTGA
 GTAGGTACGTACGTCCGGATAACGTGGTCCGGTTACTCTGGTCCCGTCACTG
 1451 sphI,

FIG. 4D

REPLACEMENT SHEET

1503 IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro
 ATAGCAGGAACACTACTAGTACCCCTCAGGAACAAATAGGATGGATGACAAATAATCCACCT
 TATCGTCCTTGATGATCATGGAAAGTCCTGTTATCCTACCTACTGTTATTAGGTGGA
 1563 IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg
 ATCCCAGTAGGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGA
 TAGGGTCATCCTCTTGTAGATATTTCTACCTATTAGGACCCATAATTATTTATCATTCT
 1623 MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp
 ATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCCTTAGAGAT
 TACATATCGGGATGGTCGTAAGACCTGTATTCTGGTCTGGTTCTGGAAATCTCTA
 1636 bstXI,
 1683 TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn
 TATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAAACAGCTTCACAGGATGTAAGAAAAT
 ATACATCTGGCCAAGATATTTGAGATTCTCGGCTTGTCAAGTGTCTACATTTTTA
 1720 hindIII,
 1743 TrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys
 TGGATGACAGAAACCTTGTGTCACAAACCCAGATTGTAAGACTATTTAAAAA
 ACCTACTGTCTTGGAACACCAGGTTTACGTTGGGTCTAACATTCTGATAAAATTT
 1796 aha111,
 1803 AlaLeuGlyProAlaAlaAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGly
 GCATTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGGGA
 CGTAACCCCTGGTCGATGTGATCTTCTTACTACTGTCGTACAGTCCCTCACCCCCCT
 1827 mbolI,
 1863 ProGlyHisLysAlaArgValLeuAlaGluAlaMetSerGlnValThrAsnProAlaAsn
 CCCGGCCATAAAAGCAAGAGTTTGGCTGAAGCCATGAGCCAAGTAACAAATCCAGCTAAC
 GGGCCGGTATTCGTTCTCAAAACCGACTTCGGTACTCGGTTATTGTTAGGTCGATTG
 p18
 1923 IleMetMetGlnArgGlyAsnPheArgAsnGlnArgLysThrValLysCysPheAsnCys
 ATAATGATGCAGAGAGGCATTTAGGAACCAAAGAAAGACTGTTAAGTGTTCATTGT
 TATTACTACGTCTCTCCGTTAAATCCTGGTTCTTGACAATTACAAAGTTAAC
 1983 GlyLysGluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysGlyCysTrpArg
 GGCAAAAGAAGGGCACATAGCCAAAAATTGCAAGGGCCCTAGGAAAAGGGCTGTTGGAGA
 CCGTTCTCCGTATCGGTTAAACGTCCGGGATCCTTTCCGACAACCTCT
 2014 apal, 2019 avr2,
 2043 CysGlyArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGly
 TGTGGAAGGGAGGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTAGGG
 ACACCTTCCCTTCTGTGGTTACTTCTAACGTGACTCTGTCCGATTAAAAATCCC
 2102 mbolI,
 2103 LysIleTrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluPro
 AAGATCTGGCCTTCCCTACAAGGGAGGGCAAGGGATTTCAGAGCAGACCCAGAGCCA
 TTCTAGACCGGAAGGGATGTTCCCTCCGGTCCCTAAAGAAGTCTCGTCTGGTCTCGGT
 2104 bg111, 2141 mbolI,

FIG. 4E

REPLACEMENT SHEET

2163 ThrAlaProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLys
 ACAGCCCCACCAGAAGAGAGCTCAGGTTGGGGAGGAGAAAACAACCTCCCTCTCAGAAC
 TGTCGGGGTGGCTTCTCTCGAACGTCAAACCCCTCCCTTTGTTGAGGGAGAGTCTTC
 2175 mb011,

2223 GlnGluProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsn
 CAGGAGCCGATAGACAAGGAACGTGATCCTTAACCTCCCTCAGATCACTCTTGGCAAC
 GTCCCTGGCTATCTGTTCTGACATAGGAAATTGAAGGGAGCTAGTGAGAAACCGTTG
 2283 AspProSerSerGlnOC
 GACCCCTCGTCACAATAAGGATAGGGGGGCAACTAAAGGAAGCTCTATTAGATAACAGGA
 CTGGGGAGCAGTGTATTCCATCCCCCGTTGATTCCTCGAGATAATCTATGTCTCCT

2342 MetAsnLeuProGlyLysTrpLysProLysMetIle
 GCAGATGATACAGTATTAGAAGAAATGAATTGCCAGGAAAATGGAAACCAAAATGATA
 CGTCTACTATGTCTAAATCTTACTTAAACGGTCCTTACCTTTACCTTGGTTTACTAT
 2360 mb011, 2375 bstXI,

2402 GlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGlnIleProValGluIleCys
 GGGGGATTGGAGGTTTATCAAAGTAAGACAGTACGATCAGATACCTGTAGAAATCTGT
 CCCCTTAACCTCCAAAATAGTTCATCTGTCTAGTCTATGGACATCTTAGACA

2462 GlyHisLysAlaIleGlyThrValLeuValGlyProThrProValAsnIleIleGlyArg
 GGACATAAAGCTATAGGTACAGTATTAGTAGGGACCTACACCTGTCAACATAATTGGAAAGA
 CCTGTATTCGATATCCATGTCTAAATCATCCTGGATGTGGACAGTTGTATTAAACCTCT
 2517 mb011,

2522 AsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrVal
 AATCTGTTGACTCAGATTGGTTGACTTTAAATTCCCCTTACCTAGTCCTATTGAAACTGTA
 TTAGACAACTGAGTCTAACCAACATGAAATTAAAGGGTAATCAGGATAACTTGACAT
 2548 ahal11, 2577 tthIII1,

2582 ProValLysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeuThrGlu
 CCAGTAAAATTAAAGCCAGGAATGGATGGCCAAAAGTTAACGAAATGGCCATTGACAGAA
 GGTCTTTAATTCGGTCCTTACCTACCGGGTTTCAATTGTTACCGGTAACGTCT
 2627 ball, 2639 mb011,

2642 GluLysIleLysAlaLeuValGluIleCysThrGluMetGluLysGluGlyLysIleSer
 GAAAAAAATAAAAGCATTAGTAGAGATATGTACAGAAATGGAAAAGGAAGGGAAAATTCA
 CTTTTTATTTCGTAATCATCTCTACATGTCTTACCTTTCCCTTAAAGT

2702 LysIleGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysAspSer
 AAAATTGGGCCTGAAAATCCATACAATACTCCAGTATTGCTATAAGAAAAAGACAGT
 TTTAACCCGGACTTTAGGTATGAGGTCTAAACGATAATTCTTTCTGTC
 2759 scal,

2762 ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp
 ACTAAATGGAGAAAATGTTAGGATTTCAAGAGAACCTAATAAGAAACTCAAGACTCTGG
 TGATTTACCTCTTGTATCATCTAAAGTCTTGAATTATTTCTTGAGTTCTGAAGACC

2822 GluValGlnLeuGlyIleProHisProGlnGlyOC
 GAAGTTCAAGTCTTATGGTGTGGCGTCCAAATTCTTTAGTCATTGTCAT

FIG. 4F

REPLACEMENT SHEET

2882 TTGGATGTGGGTGATGCATACTTTCAGTCCCTAGATAAAGACTTAGAAAGTATACTG
AACCTACACCCACTACGTATGAAAAGTCAAGGGATCTATTCTGAAATCTTCATATGAC
2895 ava3,

2943 CATTACCATACTAGTATAAACATGAGACACCAGGGATTAGATATCAGTACAATGTGG
GTAATGGTATGGATCATATTGTTACTCTGGTCCCTAATCTATAGTCATGTTACACC
2985 ecor5,

3003 LeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeu
CTGCCACAGGGATGGAAAGGATCACAGCAATATTCCAAAGTAGCATGACAAAAATCTTA
GACGGTGTCCCTACCTTCTAGTGGTCGTATAAGGTTCATCGTACTGTTTTAGAAT
3003 tthIIII, 3006 bstXI, 3021 binI,

3063 GluProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr
GAGCCTTTAGAAAAACAGAACATCCAGACATAGTTATCTATCAATACATGGATGATTGTAT
CTCGGAAAATCTTTGCTTAGGTCTGTATCAATAGATAGTTATGTACCTACTAAACATA

3123 ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHis
GTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAAAAATAGAGGAACGTGAGACAGCAT
CATCCTAGACTGAATCTTATCCCGTCGTATCTGTTTTATCTCCCTGACTCTGTCGTA
3126 binI, 3171 tthIIII,

3183 LeuLeuArgTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeu
CTGTTGAGGTGGGGATTACACACCCAGACAAAAACATCAGAAAGAACCTCCATTCC
GACAACCTCCACCCCTAAATGGTGTGGCTGTTTTGTAGTCTTCTTGAGGTAAGGAA
3234 bstXI,

3243 TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGlu
TGGATGGGTTATGAACCTCCATCCTGATAAAATGGACAGTACAGCCTATAATGCTGCCAGAA
ACCTACCCAAATACTTGAGGTAGGACTATTACCTGTATGTCGGATATTACGACGGTCTT

3303 LysAspSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer
AAAGACAGCTGGACTGTCAATGACATACAGAAGTTAGTGGAAATTGAATTGGCAAGT
TTCTGTCGACCTGACAGTTACTGTATGTCTCAATCACCCCTTAACCTAACCGTTCA
3308 pvuI,

3363 GlnIleTyrAlaGlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyThrLysAla
CAGATTATGCAGGGATTAAAGTAAAGCAGTTATGTAACCTCTAGAGGAACCAAAGCA
GTCTAAATACGTCCTAAATTCTTCGTCAATACATTGAGGAATCTCTGGTTTCGT

3423 LeuThrGluValIleProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGlu
CTAACAGAAGTAATACCAACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAG
GATTGTCTTCATTATGGTATTGTCTTCTCGTCTCGATCTGACCGTCTTGTCCCTC
3447 mboll,

3483 IleLeuLysGluProValHisGluValTyrTyrAspProSerLysAspLeuValAlaGlu
ATTCTAAAAGAACCACTACATGAAGTATATTGACCCATCAAAGACTTAGTAGCAGAA
TAAGATTTCTGGTCATGACTTCATATAACTGGTAGTTCTGAATCATCGTCTT

3543 IleGlnLysGlnGlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsn
ATACAGAAGCAGGGCAAGGCCATGGACATATCAAATTATCAAGAGGCCATTAAAAAT
TATGTCTCGTCCCCGTTCCGGTTACCTGTATAGTTAAATAGTTCTCGGTAAATTNTTA
3594 ahal11,

FIG. 4G

REPLACEMENT SHEET

3603 LeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeu
 CTGAAACAGGAAAGTATGCAAGGATGAGGGGTGCCAACACTAATGATGTAACAGTTA
 GACTTTGTCTTCATACGTTCTACTCCCCACGGGTGTGATTACTACATTTGTCAT
 3659 hpa1,
 3663 ThrGluAlaValGlnLysValSerThrGluSerIleValIleTrpGlyLysIleProLys
 ACAGAGGCAGTGCAAAAAGTATCCACAGAAAGCATAGTAATATGGGAAAGATTCTAA
 TGTCTCGTCACGTTTCATAGGTGTCTTCGTATCATTATAACCCCTTCTAAGGATT
 3723 PheLysLeuProIleGlnLysGluThrTrpGluAlaTrpTrpMetGluTyrTrpGlnAla
 TTTAAACTACCCATACAAAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCT
 AAATTGATGGGTATGTTCTTGTACCCCTCGTACCACCTACCTCATAACCGTCGA
 3723 ahal11,
 3783 ThrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGln
 ACCTGGATTCTGAGTGGGAGTTGTCAATACCCCTCCCTAGTGAAATTATGGTACCAAG
 TGGACCTAAGGACTCACCCCTAAACAGTTATGGGGAGGGAAACTTAATAACCATGGTC
 3835 kpn1,
 3843 LeuGluLysGluProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArg
 TTAGAGAAAGAACCCATAGTAGGAGCAGAAACTTCTATGTAGATGGGGCAGCTAATAGG
 AATCTCTTCTGGGTATCATCCTCGTCTTGTAAAGATACTACCCCGTCGATTATCC
 3903 GluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSer
 GAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAAGTTGTCCTCC
 CTCTGATTTAATCCTTCTCGTCTATAACATGACTGTCCTCTGTTTCAACAGAGG
 3943 mboll,
 3963 IleAlaAspThrThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAsp
 ATAGCTGACACAACAAATCAGAAGACTGAATTACAAGCAATTCTAGCTTGCAGGAT
 TATCGACTGTGTTAGTCTCTGACTTAATGTTCTGTTAAGTAGATCGAACGTCCTA
 3983 mboll,
 4023 SerGlyLeuGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAla
 TCAGGGATTAGAAGTAAACATAGTAACAGACTCACAAATATGCATTAGGAATCATTCAAGCA
 AGCCCTAATCTTCATTGTATCATTGTCTGAGTGTACGTAATCCTTAGTAAGTTCGT
 4060 ava3,
 4083 GlnProAspLysSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLysLys
 CAACCAAGATAAGAGTGAATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAAATAAAAG
 GTTGGTCTATTCTCACTTAGTCTCAATCAGTCAGTTATTATCTCGTCAATTATTTTC
 4143 GluLysValTyrLeuAlaTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnVal
 GAAAAGGTCTACCTGGCATGGGACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTA
 CTTTCCAGATGGACCCTACCCATGGTCGTGTTCTTAACCTCCTTACTTGTTCAT
 4163 kpn1,
 4203 AspLysLeuValSerAlaGlyIleArgLysValLeuPheLeuAsnGlyIleAspLysAla
 GATAAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTGAATGGAATAGATAAGGCC
 CTATTTAATCAGTCACGACCTTAGTCCTTCATGATAAAAACCTACCTTATCTATTCCGG
 4232 scal,

FIG. 4H

REPLACEMENT SHEET

4263 GlnGluGluHisGluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeu
 CAAGAAGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTAAACCTG
 GTTCTTCTTGTACTCTTATAGTGTCACTAACCTCTCGTTACCGATCACTAAAATTGGAC
 4266 mboll,

4323 ProProValValAlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGlu
 CCACCTGTAGTAGCAAAGAAATAGTAGCCAGCTGTGATAATGTCAGCTAAAAGGAGAA
 GGTGGACATCATCGTTCTTATCATCGGTCGACACTATTTACAGTCGATTTCCTCTT
 4352 pvuII,

4383 AlaMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeu
 GCCATGCATGGACAAGTAGCTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTA
 CGGTACGTACCTGTTCATCTGACATCAGGTCTTATACC GTT GATCTAACATGTGTA
 4386 ava3, 4410 bstXI, 4439 xbaI,

4443 GluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIleGluAlaGluVal
 GAAGGAAAAATTATCCTGGTAGCAGTTATGTAGCCAGTGGATATAGAAGCAGAAGTT
 CTTCCTTTAAAGGACCATCGTCAAGTACATCGGTACCTATATATCTCGTCCAA
 4497 xmn1,

4503 IleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeuAlaGlyArgTrp
 ATTCCAGCAGAGACAGGGCAGGAAACAGCATATTTCTCTAAATTAGCAGGAAGATGG
 TAAGGTCGTCTCTGTCCGTCTTGTGTATAAAAGAGAATTAAATCGTCCTTCTACC
 4555 mboll, 4560 ball,

4563 ProValLysThrIleHisThrAspAsnGlySerAsnPheThrSerThrThrValLysAla
 CCAGTAAAAACAATACATACAGACAATGGCAGCAATTTCACCAGTACTACGGTTAAGGCC
 GGTCATTTGTATGTCTGTGTTACCGTGTAAAGTGGTATGATGCCATTCCGG
 4605 scal,

4623 AlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGln
 GCCTGTTGGTGGCAGGGATCAAGCAGGAATTGGCATTCCCTACAATCCCCAAAGTC
 CGGACAACCACCGTCCTAGTTCGTCTAAACGTAAGGGATGTTAGGGGTTTCAGTT
 4639 binI,

4683 GlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGln
 GGAGTAGTAGAATCTATGAATAATGAATTAAAGAAAATTATAGGACAGGTAAAGAGATCAG
 CCTCATCATCTTAGATACTTATTACTTAATTCTTTAATATCCTGTCCATTCTCTAGTC

4743 AlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLys
 GCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCACAATTAAAGAAAA
 CGACTTGGGAATTCTGTGTCATGTGTAAAGTAGGTGTTAAATTTCTTT
 4752 alf11, 4791 ahall11,

4803 GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIle
 GGGGGGATTGGGGGATACAGTGCAGGGAAAGAATAGTAGACATAATAGCAACAGACATA
 CCCCCCTAACCCCTATGTCACGTCCCTTCTTATCATCTGTATTATCGTTGTCTGTAT

4863 GlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArg
 CAAACTAAAGAAACTACAAAAGCAAATTACAAAATTCAATTTCGGGTTTATTACAGG
 GTTGATTCTTGTGTTAGTTAAGTTAAAAGCCAAATAATGTCC

FIG. 41

REPLACEMENT SHEET

4923 AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAla
 GACAACAAAGATCCCCTTGGAAAGGACCAGCAAAGCTCTGGAAAGGTGAAGGGGGCA
 CTGTTGTTCTAGGGAAACCTTCCTGGCGTTCGAAGAGACCTTCACTTCCCCGT

4956 hindIII,

4983 ValValIleGlnAspAsnSerAspIleLysValValProArgArgLysAlaLysIleIle
 GTAGTAATAACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAAATCATT
 CATCATTATGTTCTATTACTGTATTTCATCACGGTTCTCTTTGTTAGTAA

5023 mbolI,

5043 MetGluAsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIle
 ArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArgGlnAspGluAsp
 AGGGATTATGGAAAAACAGATGGCAGGTGATGATTGTGGCAAGTAGACAGGATGAGGGAT
 TCCCTAACCTTTGTCTACCGTCCACTACTAACACACCGTCATCTGCCACTCCTA

5103 ArgTreTrpLysSerLeuValLysHisHisMetTyrIleSerLysLysAlaLysGlyTrp
 AM
 TAGAACATGGAAAAGTTAGTAAAACACCATATGTATATTCAAAGAAAAGCTAAAGGATGG
 ATCTTGTACCTTTCAAATCATTTGTGGTACATATAAAAGTTCTTCGATTTCTTAC

5131 ndel,

5163 PheTyrArgHisHisTyrGluSerThrHisProArgValSerSerGluValHisIle
 TTTTATAGACATCACTATGAAAGTACTCATCCAAGAGTAAGTTCAGAAGTACACATC
 AAAATATCTGTAGTGTACATTCTGAGTAGGTTCTCATTCAAGTCTTGTGTAG

5185 scal,

5221 ProLeuGlyAspAlaLysLeuValIleThrThrTyrTrpGlyLeuHisThrGlyGluArg
 CCCCTAGGGGATGCTAAATTGGTAATAACACATATTGGGGTCTGCATACAGGAGAAAGA
 GGGGATCCCCTACGATTAAACCATTATTGTTGATAACCCCAGACGTATGTCCTTTCT

5223 avr2,

5281 GluTrpHisLeuGlyGlnGlyValAlaIleGluTrpArgLysLysLysTyrSerThrGln
 GAATGGCATTGGGCCAGGGAGTCGCCATAGAATGGAGGAAAAGAAATATAGCACACAA
 CTTACCGTAAACCGGTCCCTCAGCGGTATCTTACCTCCTTTCTTATATCGTGTGTT

5341 ValAspProGlyLeuAlaAspGlnLeuIleHisLeuHisTyrPheAspCysPheSerGlu
 GTAGACCCCTGGCCTAGCAGACCAACTAATTCACTGCATTATTGATTGTTTCAAGAA
 CATCTGGGACCGGATCGTCTGGTGTAAAGTAGACGTAAACAAACTAACAAAAAGCTT

5401 SerAlaIleLysAsnAlaIleLeuGlyTyrArgValSerProArgCysGluTyrGlnAla
 TCTGCTATAAAATGCCATTAGGATAAGAGTTAGTCTAGGTGTGAATATCAAGCA
 AGACGATATTACGGTATAATCCTATATCTCAATCAGGATCCACACTTATAGTCGT

5440 avr2,

5461 GlyHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuAlaLeuIleThrProLys
 GGACATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTAAACACCAAAA
 CCTGTATTGTTCCATCCTAGAGATGTTAGAACCGTGATCGTCGTAAATTATTGTGGTTT

5476 binI,

5521 LysThrLysProProLeuProSerValLysLysLeuThrGluAspArgTrpAsnLysPro
 AAGACAAAGCCACCTTGCCTAGTGTAAAGAAACTGACAGAGGATAGATGGAACAAGCCC
 TTCTGTTCGGTGGAAACGGATCACAATTCTTGACTGTCTCCTATCTACCTTGTTCGGG

FIG. 4J

REPLACEMENT SHEET

5581 GlnLysThrLysGlyHisArgGlySerHisThrMetAsnGlyHisAM
 CAGAAGACCAAGGGCACAGAGGGAGCCATACAATGAATGGACACTAGAGCTTTAGAGG
 GTCTTCTGGTTCGGTGTCTCCCTCGGTATGTTACCTGTGATCTCGAAAATCTCC
 5583 mbo11,
 5641 AGCTTAAGAGAGAACGCTGTTAGACATTTCTAGGCCATGGCTCCATAGCTTAGGACAAT
 TCGAATTCTCTTCGACAATCTGAAAGGATCCGGTACCGAGGTATCGAATCCTGTTA
 5643 af111, 5670 avr2, 5676 ncol,
 5701 ATATCTATGAAACTTATGGGGATACTGGGCAGGAGTGGAAAGCCATAATAAGAATTCTGC
 TATAGATACTTGAATACCCCTATGAACCCGTCTCACCTCGGTATTATTCTTAAGACG
 5752 ecor1,
 5761 AACAACTGCTTTATTCACTTCAAGATTGGGTGTCAACATAGCAGAACATAGGCATTATTC
 TTGTTGACGACAAATAAGTAAAGTCTTAACCCACAGTTGATCGTCTTATCCGTAATAAG
 5821 AACAGAGGAGAGCAAGAAGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAAGCAT
 TTGTCCTCTCGTTCTTACCTCGGTATCTAGGATTAGATCTCGGACCTCGTA
 5836 mbo11, 5862 xba1,
 5881 CCAGGAAGTCAGCCTAGGACTGCTGTAACAATTGCTATTGAAAAAGTGGCTTTCAT
 GGTCTTCAGTCGGATCCTGACGAACATTGTTAACGATAACATTTCACAACGAAAGTA
 5893 avr2,
 5941 TGCTACCGCGTGTTCACAAGAAAAGGCTAGGCATCTCCTATGGCAGGAAGAACGGAGA
 ACGATGCGCACAAAGTGTCTTCCGAATCCGTAGAGGATACCGTCTTCTCGCCTCT
 5945 mlu1, 5988 mbo11,
 6001 CAGCGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTTCTATCAAAGCAGTAA
 GTCGCTCTCGAGGAGTCCTGTCAGTCTGAGTAGTTGAAGAGATAGTTCTGTCATT
 6008 mbo11, 6011 sac1, 6016 mstII, 6038 hindIII,
 6061 GTAGTAAATGTAATGCAATCTTACAAATATTAGCAATAGTATCATTAGTAGTAGCA
 CATCATTACATTAGTTAGAAATGTTATAATCGTTATCATAGTAATCATCATCGT
 6121 ATAATAGCAATAGTTGTGGACCATAGTACTCATAGAATATAGGAAATATTAAGACAA
 TATTATCGTTATCAACACACCTGGTATCATGAGTATCTTATATCCTTTATAATTCTGTT
 6147 sca1,
 6181 AGAAAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAACAGCTGGCAATGAAA
 TCTTTATCTGTCTAATTAACATCTTATTCTCTTCTGTCTGTACCGTTACTTT
 6222 mbo11,
 6241 ValLysGlyThrArgArgAsnTyrGlnHisLeuTrpArgTrpGlyThrLeuLeuLeuGly
 GTGAAGGGGACCAGGAGGAATTATCAGCACTTGAGGAGATGGGGCACCTTGCTCCTGGG
 CACTTCCCTGGTCTCCTTAATAGTCGTAAACACCTACCCCCGTGGAACGAGGAACCC
 MetLeuMetIleCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValPro
 6301 ATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTACAGTTATTATGGAGTACCT
 TACAACCTAGACATCACGATGTCTTTAACACCCAGTGTCAAATAACCTCATGGA

MetLys ENV

FIG. 4K

REPLACEMENT SHEET

6361 ValTrpLysGluAlaThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThr
 GTGTGGAAAGAAGCAACTACCACTCTATTGTGCATCAGATGCTAGAGCATATGATA
 CACACCTTCCTCGTTGAGATAAAACACGTAGTCTACGATCTCGTATACTATGT
 6410 ndel,
 GluValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGlu
 6421 GAGGTACATAATGTTGGCCACACATGCTGTACCCACAGACCCCAACCCACAAGAA
 CTCCATGTATTACAAACCCGGTGTGTACGACACATGGGTGTCTGGGTTGGTCTT
 ValValLeuGlyAsnValThrGluAsnPheAsnMetTrpLysAsnAsnMetValGluGln
 6481 GTAGTATTGGGAAATGTGACAGAAAATTAAACATGTGGAAAAATAACATGGTAGAACAG
 CATCATAACCCTTACACTGTCTTTAAAATTGTACACCTTTATTGTACCATCTTGC
 MetGlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThr
 6541 ATGCAGGAGGATATAATCAGTTATGGGATCAAAGCCTAAAGCCATGTGAAAATTAAAC
 TACGTCTCCTATATTAGTCAAATACCTAGTTGGATTTCGGTACACATTAAATTGG
 6567 binI,
 ProLeuCysValThrLeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSer
 6601 CCACTCTGTGTTACTTTAAATTGCACTGATTGGGAAGGCTACTAATACCAATAGTAGT
 GGTGAGACACAATGAAATTAAACGTGACTAAACCCCTCCGATGATTATGGTTATCATCA
 6615 ahal11,
 AsnTrpLysGluGluIleLysGlyGluIleLysAsnCysSerPheAsnIleThrThrSer
 6661 AATTGGAAAGAAGAAATAAAAGGAGAAATAAAACTGCTCTTCAATATCACCACAAGC
 TTAACCTTCTTCTTATTTCCTCTTATTGGTACGAGAAAGTTAGTGGTCTCG
 6670 mbo11,
 IleArgAspLysIleGlnLysGluAsnAlaLeuPheArgAsnLeuAspValValProIle
 6721 ATAAGAGATAAGATTCAAGAAAATGCACTTTTCGTAACCTGATGTAGTACCAATA
 TATTCTCTATTCTAACGTCTTACGTGAAAAGCATTGGAACATCATCATGGTTAT
 AspAsnAlaSerThrThrAsnTyrThrAsnTyrArgLeuIleHisCysAsnArgSer
 6781 GATAATGCTAGTACTACTACCAACTATACCAACTATAGGTTGATACATTGTAACAGATCA
 CTATTACGATCATGATGATGGTTGATATGGTTGATATCCAACATATGTAACATTGTCTAGT
 6790 scal,
 ValIleThrGlnAlaCysProLysValSerPheGluProIleProIleHisTyrCysThr
 6841 GTCATTACACAGGCCGTGTCAGGTTATCATTGAGCCAATTCCCATAACATTATGGTAC
 CAGTAATGTTGCGACAGGTTCCATAGTAAACTCGGTTAAGGGTATGTAATAACATGG
 6851 stu1,
 ProAlaGlyPheAlaIleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCys
 6901 CGGGCTGGTTTGCATTCTAAAGTGTAAATAATAAAACGTTCAATGGAAAAGGACCATGT
 GGCCGACCAAAACGCTAACGATTACATTATTGGTCAAGTTACCTTCTGGTACA
 ThrAsnValSerThrValGlnCysThrHisGlyIleArgProIleValSerThrGlnLeu
 6961 ACAAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTG
 TGTTTACAGTCGTGTCATGTTACATGTGTACCTTAATCGGTTATCACAGTTGAGTTGAC
 LeuLeuAsnGlySerLeuAlaGluGluValValIleArgSerAspAsnPheThrAsn
 7021 CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACGAA
 GACAATTACCGTCAGATCGTCTTCTCCATCATTAACTAGACTGTTAAAGTGCTTG
 7042 mbo11, 7045 mbo11, 7060 bg111,

FIG. 4L

REPLACEMENT SHEET

7081 AsnAlaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgPro
 AATGCTAAAACCATAATTAGTACAGCTGAATGAATCTGTAGCAATTAACTGTACAAGACCC
 TTACGATTTGGTATTATCATGTCGACTTACTTAGACATCGTTATTGACATGTTCTGGG
 7102 pVull,

 7141 AsnAsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAlaPheHisThrThrGly
 AACAAACAATAAAGAAAAAGTATCTATATAGGACCAGGGAGAGCATTCTACAAACAGGA
 TTGTTGTTATGTTCTTTCTAGATATACTCTGGTCCCTCTCGTAAAGTAAGTGTGCT
 7199 mbol1,

 7201 ArgIleIleGlyAspIleArgLysAlaHisCysAsnIleSerArgAlaGlnTrpAsnAsn
 AGAATAATAGGAGATAAAGAAAAGCACATTGTAACATTAGTAGAGCACAATGGAATAAC
 TCTTATTATCCTCTATATTCTTGTAACTTGTAATCATCTCGTGTACCTTATTG

 7261 ThrLeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsnAsnLysThrIleVal
 ACTTTAGAACAGATAGTTAAAAAAATTAAAGAGAACAGTTGGGAATAATAAAACAATAGTC
 TGAAATCTGTCTATCAATTTTAATTCTCTGTCAAACCCATTATTATTGTTATCAG

 7321 PheAsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGly
 TTTAATCAATCCTCAGGAGGGGCCAGAAATTGTAATGCACAGTTTAATTGTAGAGGG
 AAATTAGTTAGGAGTCCTCCCTGGGTCTTAACATTACGTGTCAAAATTAAACATCTCCC
 7331 mstII,

 7381 GluPhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThr
 GAATTTTTCTACTGTAATAACACACAACGTTAAATAACATGGAGGTAAATCACACT
 CTTAAAAAGATGACATTATGTTGTTGACAAATTATTATGTAACCTCCAATTAGTGTGA

 7441 GluGlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsn
 GAAGGAACTAAAGGAATGACACAATCATACTCCCAGTGAATAAAACAAATTATAAAC
 CTTCCTTGATTTCTTACTGTGTTAGTATGAGGGTACATCTTATTGTTAAATTG

 7501 MetTrpGlnGluValGlyLysAlaMetTyrAlaProProlleGlyGlyGlnIleSerCys
 ATGTGGCAGGAAGTAGGGAAAAGCAATGTATGCCCTCCATTGGAGGACAAATTAGTGT
 TACACCGTCCTCATCTTGTACATACGGGGAGGGTAAACCTCTGTTAAATCAACA

 7561 SerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAsp
 TCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTACAAATGTAACATGAC
 AGTAGTTATAATGTCCCAGCATAATTGTTCTTACACCACATGTTACATTGATTACTG

 7621 ThrGluValPheArgProGlyGlyAspMetArgAspAsnTrpArgSerGluLeuTyr
 ACCGAGGTCTTCAGACTGGAGGAGGATATGAGGGACAATTGGAGAAGTGAATTATAT
 TGGCTCCAGAAGTCTGGACCTCCTCTATACTCCCTGTTAACCTCTTACCTTAATATA
 7628 mbol1,

 7681 LysTyrLysValIleLysIleGluProLeuGlyIleAlaProThrLysAlaLysArgArg
 AAATATAAAGTAATAAAATTGAACCATTAGGAATAGCACCCACCAAGGCAAGAGAAAGA
 TTTATATTCATTATTAACTGGTAATCCTTATCGTGGTGGTCCGTTCTCTCT
 7736 mbol1,

 7741 ValValGlnArgGluLysArgAlaValGlyIleValGlyAlaMetPheLeuGlyPheLeu
 GTGGTGCAGAGAGAAAAAGAGCAGTGGGAATAGTAGGAGCTATGTTCTGGGTTCTG
 CACCACGTCTCTCTTCTCGTACCCATTATCCTCGATAACAAGGAACCCAAGAAC

 7801 GlyAlaAlaGlySerThrMetGlyAlaValSerLeuThrLeuThrValGlnAlaArgGln
 GGAGCAGCAGGAAGCACTATGGGCGCAGTGTCAATTGACGCTGACGGTACAGGCCAGACAA
 CCTCGTCGTCCTCGTACCCCGCTCACAGTAACTGCGACTGCCATGTCGGTCTGTT

FIG. 4M

REPLACEMENT SHEET

7861 LeuLeuSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGln
 TTATTGTCTGGTATAGTGCACACAGCAGAACAAATTGCTGAGGGCTATTGAGGCGCAACAA
 AATAACAGACCATATCACGTTGTCGTTAAACGACTCCGATAACTCCGCGTTGTT

 7921 HisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
 CATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTG
 GTAGACAACGTTGAGTGTCAAGACCCCGTAGTTGTCGAGGTCCGTTCTCAGGACCGACAC

 7981 GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
 GAAAGATACTTAAGGGATCAACAGCTCTAGGGATTGGGGTTGCTCTGGAAAACCTCATT
 CTTCTATGGATTCC[^]CTAGTTGTCGAGGATCCCTAAACCCCAACGAGACCTTTGAGTAA

 7989 mstII, 7995 binI, 8007 avr2,

 8041 CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
 TGCAACACTGCTGTGCCCTGGAAATGCTAGTTGGAGTAATAATCTCTGGAAAGACATTGG
 ACGTGGTGACGACACGGAACCTTACGATCACCTCATTATTAGAGAC[^]TTCTGTAAACC

 8089 mbolI,

 8101 AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
 GATAAACATGACCTGGATGCAGTGGAAAGAGAAATTGACAATTACACAAACACAATATAC
 CTATTGACTGGACCTACGTCAACCTTCTTTACTGTTAATGTGTTGTATATG

 8161 ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
 ACCTTACTTGAAGAACGAGATCGCAGAACCAACAAGAAAAGAATGAACAAGAATTATTAGAATTG
 TGGAATGAACTTCTTAGCGTCTGGTTCTTTCTTACTTGTCTTAATAATCTAAC

 8170 mbolI,

 8221 AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpLeuTrpTyrIleLys
 GATAAGTGGGCAAGTTGTGGAATTGGTTAGCATAACAAACTGGCTGTGGTATATAAAG
 CTATTCCCCGTTCAAACACCTAACCAATCGTATTGTTGACCGACACCATATATTC

 8281 IlePheIleMetIleValGlyGlyLeuValGlyLeuArgIleValPheAlaValLeuSer
 ATATTCTATAATGATAGTAGGAGGCTTGGTAGGTTAAAGAATAGTTTTGCTGTGCTTCT
 TATAAGTATTACTATCATCCTCCGAACCATCAAATTCTTATCAAAAACGACACGAAAGA

 8341 IleValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrArgLeuProVal
 ATAGTGAATAGAGTTAGGCAGGGATACTCACCATTTGCTATTTCAGACCCGCCCTCCCAGTC
 TATCACTTATCTCAATCCGTCCCTATGAGTGGTAACAGTAAAGTCTGGGCGGAGGGTCAG[^]

 8400 aval,

 8401 ProArgGlyProAspArgProAspGlyIleGluGluGluGlyGlyGluArgAspArgAsp
 CCGAGGGGACCCGACAGGCCGACGGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGAGAC
 GGCTCCCTGGGCTGTCCGGCTGCCTAGCTTCTTCCACCTCTCTGTCTGTC

 8431 mbolI, 8434 mbolI,

 8461 ArgSerValArgLeuValAspGlyPheLeuAlaLeuIleTrpGluAspLeuArgSerLeu
 AGATCCGTTGATTAGTGGATGGATTCTTAGCACTTATCTGGGAAAGATCTGCGGAGCCTG
 TCTAGGCAAGCTAACCTACCTAACGTAAGAATCGTAAGACCC[^]TTAGACGCCTCGGAC

 8503 mbolI, 8505 bgI11,

 8521 CysLeuPheSerTyrArgArgLeuArgAspLeuLeuLeuIleAlaAlaArgThrValGlu
 TGCCTCTTCAGCTACCGCCGCTTGAGAGACTTACTCTGATTGCAGCGAGGACTGTGGAA
 ACGGAGAACGTCGATGGCGCGAACCTCTGAATGAGAAACTAACGTCGCTCTGACACCTT

 8525 mbolI,

FIG. 4N

REPLACEMENT SHEET

8581 IleLeuGlyHisArgGlyTrpGluAlaLeuLysTyrTrpTrpSerLeuLeuGlnTyrTrp
 ATTCTGGGGCACAGGGGTGGGAAGCCCTCAAATATTGGTGGAGTCTCCTGCAGTATTGG
 TAAGACCCCGTGTCCCCACCCCTCGGGAGTTATAACCACCTCAGAGG~~G~~ACGTCAAAAC
 8629 pst1,
 IleGlnGluLeuLysAsnSerAlaValSerTrpLeuAsnAlaThrAlaIleAlaValThr
 8641 ATTCAAGGAACTAAAGAATAGTGTGTTAGCTGGCTAACGCCACAGCTATAGCAGTAAC
 TAAGTCCTTGATTTCTTATCACGACAATCGACCGAGTTGCGGTGTCGATATCGTCATTGA
 GluGlyThrAspArgValIleGluValAlaGlnArgAlaTyrArgAlaIleLeuHisIle
 8701 GAGGGGACAGATAGGGTTATAGAAGTAGCACAAAGAGCTTATAGAGCTATTCTCACATA
 CTCACCTGTCTATCCAAATATCTCATCGTGTTCGAAATATCTCGATAAGAGGTGTAT
 HisArgArgIleArgGlnGlyLeuGluArgLeuLeuOC MetGlyGlyLysTrpSer
 8761 CATAGAAGAATTAGACAGGGCTTGGAAAGGCTTTGCTATAAGATGGGTGGCAAGTGGTCA
 GTAT~~C~~TCTTAATCTGCCCCAACCTTCCGAAACGATATTCTACCCACCGTTACCAAGT
 8765 mbo11,
 LysArgSerMetGlyGlyTrpSerAlaIleArgGluArgMetArgArgAlaGluProArg
 8822 AAACGTAGTATGGGTGGATGGTCTGCTATAAGGGAAAGAATGAGACGAGCTGAGCCACGA
 TTTGCATCATACCCACCTACCAGACGATATTCCCTTACTCTGCTGACTCGGTGCT
 AlaGluProAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAla
 8882 GCTGAGGCCAGCAGCAGATGGGTGGAGCAGTATCTGAGACCTGGAAAAACATGGAGCA
 CGACTCGGTCGTCGTCTACCCACCCACCGTCA~~TA~~AGAGCTCTGGACCTTTGTACCTCGT
 8883 tthIII1, 8916 aval xhol,
 IleThrSerSerAsnThrAlaAlaThrAsnAlaAspCysAlaTrpLeuGluAlaGlnGlu
 8942 ATCACAAAGTAGCAATAACAGCAGCTACTAATGCTGATTGTCGCTGGCTAGAACGACAAGAG
 TAGTGTTCATCGTTATGTCGTCGATGATTACGACTAACACGGACCGATCTCGTGTTC
 GluGluGluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLys
 9002 GAGGAAGAGGTGGGTTTCCAGTCAGACCTCAGGTACCTTAAAGACCAATGACTTACAAG
 CTCCTCTCCACCCAAAAGGTCAGTCTGGAGTCCATGGAAATTCTGGTTACTGAATGTT
 9005 mbo11, 9029 mstII, 9034 kpn1,
 AlaAlaLeuAspIleSerHisPheLeuLysGluLysGlyLeuGluGlyLeuIleTrp
 9062 GCAGCTTAGATATTAGCCACTTTAAAGAAAAGGGGGACTGGAAGGGCTAATTGG
 CGTCGAAATCTATAATCGGTGAA~~A~~TTTCTTCCCCCTGACCTCCGATTAAACC
 9085 aha111,
 SerGlnArgArgGlnGluIleLeuAspLeuTrpIleTyrHisThrGlnGlyTyrPhePro
 9122 TCCCAGGAAAGACAAGAGATCCTGATCTGTGGATCTACCACACACAAGGCTACTCCCT
 AGGGTTCTCTGTTCTAGGAAC~~T~~AGACACCTAGATGGTGTGTTCCGATGAAGGG
 9129 mbo11, 9153 binI,
 AspTrpGlnAsnTyrThrProGlyProGlyIleArgTyrProLeuThrPheGlyTrpCys
 9182 GATTGGCAGAATTACACACCAGGGGCCAGGGATCAGATATCCACTGACCTTGGATGGTGC
 CTAACCGTCTTAATGTTGGTCCGGTCC~~A~~TAGTCTAGGTGACTGGAAACCTACCAAC
 9210 binI, 9216 ecor5,

FIG. 4O

REPLACEMENT SHEET

9242 PheLysLeuValProValGluProGluLysValGluGluAlaAsnGluGlyGluAsnAsn
TTCAAGCTAGTACCGAGTTGAGCCAGAGAAGGTAGAAGAGGGCCAATGAAGGAGAGAACAAAC
AAGTTCGATCATGGTCAACTCGGTCTTCCAT^{CTTCTCCGGTTACTTCCTCTTTGTTG}
9275 mb011,

9302 SerLeuLeuHisProMetSerLeuHisGlyMetGluAspAlaGluLysGluValLeuVal
AGCTTGTTACACCCATGAGCCTGCATGGGATGGAGGACGCGGAGAAAGAAGTGTAGTG
TCGAACAATGTGGGATACTCGGACGTACCCCTACCTCCTCGGCCCTTTCTTCACAATCAC

9362 TrpArgPheAspSerLysLeuAlaPheHisHisMetAlaArgGluLeuHisProGluTyr
TGGAGGTTTGACAGCAAACTAGCATTACATCACATGGCCCAGAGAGCTGCATCCGGAGTAC
ACCTCCAAACTGTCGTTGATCGTAAAGTAGTGTACCGGGCTCTGACGTAGGCCTCATG
9399 aval, 9417 scal,

9422 TyrLysAspCysOP
TACAAAAGACTGCTGACATCGAGCTTCTACAAGGGACTTCCGCTGGGACTTTCCAGGG
ATGTTTCTGACGACTGTAGCTGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCC

9482 AGGC GTGGC CTGGC GGG ACTGGGAGTGGCGTCCCTCAGATGCTGC ATATAAGCAGCTG
TCCGCACCGGACCCG CCTGACCCCTCACCGCAGGGAGTCTACGACGTATATT CGTCGAC
9536 pvu11,

9542 CTTTTGCTGTACTGGGTCTCTCTGGTAGACCAGATCTGAGCCTGGAGCTCTGGC
GAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTCGGACCCCTGAGAGACCG
9576 bg111, 9590 sac1,

9602 TAACTAGGGAACCCACTGCTTAAGCCTCAATAAGCTTGCCTGAGTGCTCAAGTAGTG
ATTGATCCCTGGGTGACGAATT CGGAGTTAT^TTCGAACGGAACTCACGAAGTTCATCAC
9620 af111, 9634 hind111,

9662 TGTGCCCGTCTGTTGTGACTCTGGTAACTAGAGATCCCTCAGACCCCTTGTAGTCAGTG
ACACGGGCAGACAACACACTGAGACCAATTGATCTCTAGGGAGTCTGGAAAATCAGTCAC

9722 TGGAAAAATCTCTAGCAG
ACCTTTTAGAGATCGTC

FIG. 4P

REPLACEMENT SHEET

U3 →

-453 CTGGAAGGGCTAATTGGTCCAAAGAACAGACAAGAGATCCTGATCTGTGGATCTACACACACAAGGCTACTTCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCA

-333 CTGACCTTGGATGGTCTCAAGCTAGTACCACTGAGGCCAGAGAACGGTAGAAGAGGCC
AATGAAGGAGAGAACAAACAGCTTGTACACCCATGAGCCTGCATGGATGGAGGACGCG

L

-214 GAGAAAGAACAGTGTAGTGTGGAGGTTGACAGCAAACTAGCATTCATCACATGGCCCGA
GAGCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTCTACAAGGGACTTCCG

T

-93 CTGGGGACTTCCAGGGAGGCCTGGCCTGGCGGGACTGGGAGTGGCGTCCCTCAGATG
CTGCATATAAGCAGCTGCTTTGCCTGTACTG ←U3 R →
R

28 CCTGGGAGCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAGCTTGCCTT
GAGTGCTTCA AGTAGTGTGTGCCGTCTGTTGTGACTCTGGTAACTAGAGATCCCTCA

←R U5 →

148 GACCCTTTAGTCAGTGTGGAAAAATCTCTAGCAG TGGCGCCCGAACAGGGACGCGAAA
GCGAAAGTAGAACCAAGAGGAGCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACAG

57

268 CAAGAGGCAGGGCGCGACTGGTGAGTACGCCATTGGACTAGCGGAGGCTAGAAC
MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspLysTrpGlu
GAGAGAGAGATGGGTGCGAGAGCGTCGGTATTAGCGGGGGAGAATTAGATAATGGGAA
LysIleArgLeuArgProGlyGlyLysLysTyrLysLeuLysHisIleValTrpAla
388 AAAATTGGTTAAGGCCAGGGGAAAGAAAAATATAAGTTAAACATATAGTATGGGCA
SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
AGCAGGGAGCTAGAACGATTGCGAGTCATCCCTGGCTGTTAGAAACATCAGAAGGCTGC

97

508 ArgGlnIleLeuGlyGlnLeuGlnProSerLeuGlnThrGlySerGluGluLeuArgSer
AGACAAATATTGGGACAGCTACAGCCATCCCTCAGACAGGATCAGAAGAACTTAGATCA
LeuTyrAsnThrValAlaThrLeuTyrCysValHisGlnArgIleAspValLysAspThr
TTATATAATACAGTAGCAACCCTTATTGTGTACATCAAAGGATAGATGTAAAAGACACC

137

628 LysGluAlaLeuGluLysIleGluGluGlnAsnLysSerLysLysLysAlaGlnGln
AAGGAAGCTTAGAGAACGAGATAGAGGAAGAGCAAAACAAAGTAAGAAAAGGCACAGCAA
AlaAlaAlaAlaAlaGlyThrGlyAsnSerSerGlnValSerGlnAsnTyrProIleVal
GCAGCAGCTGCAAGCTGGCACAGGAAACAGCAGCCAGGTCAAGCCAAAATTACCTATAGTG

748 GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
CAGAACCTACAGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCATGG

177

ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
GTAAAAGTAGTAGAAGAAAAGGCTTCAGCCAGAAGTAATACCATGTTTACGCATTA

868 SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
TCAGAAGGAGCCACCCCACAAGATTAAACACCATGCTAACACAGTGGGGGACATCAA

FIG. 5A

REPLACEMENT SHEET

	AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal	217	G
	GCAGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATAGAGTG		
988	HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp CATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGGGAAAGTGAC	A	
	IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro ATAGCAGGAACACTAGTACCCCTCAGGAACAAATAGGATGGATGACAATAATCCACCT	257	
1108	IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg ATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGA	G	
	MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp ATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCCTTAGAGAT	297	
1228	TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn TATGTAGACCGGTTCTATAAAACTCTAAGAGGCCAACAGCTTCACAGGATGTAAAAAAAT		
	TrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys TGGATGACAGAAACCTTGGTCCAAAATGCAAACCCAGATTGTAAGACTATTTAAAAA	337	
1348	AlaLeuGlyProAlaAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGly GCATTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGGGGA		
	ProGlyHisLysAlaArgValLeuAlaGluAlaMetSerGlnValThrAsnProAlaAsn CCCAGGCCATAAAGCAAGAGTTTGGCTGAAGGCCATGAGCCAAGTAACAAATCCAGCTAAC	377	
1468	IleMetMetGlnArgGlyAsnPheArgAsnGlnArgLysThrValLysCysPheAsnCys ATAATGATGCAGAGAGGCAATTAGAACCAAAGAAAGACTGTTAAGTGTTCATTGT		
	GlyLysGluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysGlyCysTrpArg GGCAAAGAAGGGCACATAGCCAAAATTGCAGGGCCCCTAGGAAAAGGGCTGTTGGAGA	417	
	CysGlyArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGly PhePheArgG		
1588	TGTGGAAGGGAGGACACAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTAGGG LysIleTrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluPro IuAspLeuAlaPheLeuGlnGlyLysAlaArgGluPheSerSerGluGlnThrArgAla AAGATCTGGCCTTCTACAAGGGAGGCCAGGGATTTCAGAGCAGACCAGAGCCA	457	
	ThrAlaProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLys AsnSerProThrArgArgGluLeuGlnValTrpGlyGlyGluAsnAsnSerLeuSerGluA	23	
1708	ACAGCCCCACCCAGAAGAGAGCTTCAGGTTGGGAGGAGAAAACAACCTCCCTCAGAAC GlnGluProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsn IaGlyAlaAspArgGlnGlyThrValSerPheAsnPheProGlnIleThrLeuTrpGln	P	
	CAGGAGCCGATAGACAAGGAACCTGTATCCTTAACTTCCCTCAGATCACTCTGGCAAC	497	
	AspProSerSerGlnOC ArgProLeuValThrIleArgIleGlyGlyGlnLeuLysGluAlaLeuLeuAspThrGlyA 1828 GACCCCTCGTACAATAAGGATAGGGGGCAACTAAAGGAAGCTATTAGATACAGGAG	63	O
	IaAspAspThrValLeuGluGluMetAsnLeuProGlyLysTrpLysProLysMetIle CAGATGATACTAGTATTAGAAGAAATGAATTGCCCCAGGAAACCAAAATGGAAACCAAAATGATAG	103	L
1948	GlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGlnIleProValGluIleCysG GGGAATTGGAGGTTTATCAAAGTAAGACAGTACGATCAGATACTGTAGAAATCTGTG		

FIG. 5B

REPLACEMENT SHEET

1yHisLysAlaIleGlyThrValLeuValGlyProThrProValAsnIleIleGlyArg 143
 GACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAA
 AsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrValP
 2068 ATCTGTTGACTCAGATTGGTTGACTTTAAATTCCCCATTAGTCCTATTGAAACTGTAC
 roValLysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeuThrGlu 183
 CAGTAAAATTAAAGCCAGGAATGGATGGCCCAAAGTTAACAGCAATGCCATTGACAGAAG
 GluLysIleLysAlaLeuValGluIleCysThrGluMetGluLysGluGlyLysIleSerL
 2188 AAAAATAAAAGCATTAGTAGAGATATGTACAGAAATGGAAAAGGAAGGGAAAATTCAA
 ysIleGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSer 223
 AAATTGGGCCTGAAAATCCATACAATACTCCAGTATTGCTATAAAGAAAAAGACAGTA
 ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrpG
 2308 CTAAATGGAGAAAATAGTAGATTTCAGAGAACTTAATAAGAACTCAAGACTCTGGG
 luValGlnLeuGlyIleProHisProAlaGlyLeuLysLysLysSerValThrVal 263
 AAGTTCAAGTTAGGAATACCACACCCCGCAGGGTTAAAAAGAAAAATCAGTAACAGTAT
 LeuAspValGlyAspAlaTyrPheSerValProLeuAspLysAspPheArgLysTyrThrA
 2428 TGGATGTGGGTGATGCATACTTTCAAGTTCCCTAGATAAAGACTTAGAAAGTATACTG
 laPheThrIleProSerIleAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnVal 303
 CATTACCATACCTAGTATAAACAAATGAGACACCAGGGATTAGATATCAGTACAATGTGC
 LeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeuG
 2548 TGCCACAGGGATGGAAAGGATCACAGCAATATTCCAAGTAGCATGACAAAAATCTTAG
 luProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr 343
 AGCCTTTAGAAAACAGAAATCCAGACATAGTTATCTATCAATACATGGATTTGTATG
 ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHisL
 2668 TAGGATCTGACTTAGAAATAGGGCAGCATAGAACAAAAATAGAGGAACGTGAGACAGC
 euLeuArgTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeu 383
 TGTTGAGGTGGGGATTACACACCAGACAAAAAACATCAGAAAGAACCTCCATTCC
 TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGluL
 2788 GGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAAA
 ysAspSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer 423
 AAGACAGCTGGACTGTCAATGACATACAGAAGTTAGTGGAAAATTGAATTGGCAAGTC
 GlnIleTyrAlaGlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyThrLysAlaL
 2908 AGATTATGCAGGGATTAAAGTAAAGCAGTTATGAAACTCCTTAGAGGAACCAAAGCAC
 euThrGluValIleProLeuThrGluGluAlaGluLeuGluAlaGluAsnArgGlu 463 P
 TAACAGAAGTAATACCACTAACAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAGA
 IleLeuLysGluProValHisGluValTyrTyrAspProSerLysAspLeuValAlaGluI
 3028 TTCTAAAAGAACCACTGACATGAAGTATATTGACCCATCAAAAGACTTAGCAGAAA
 leGlnLysGlnGlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsn 503 O
 TACAGAACAGGGCAAGGCCATGGACATATCAAATTATCAAGAGCCATTAAAAATC
 LeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeuT
 3148 TGAAAACAGGAAAGTATGCAAGGATGAGGGTGCCCACACTAATGATGAAACAGTTAA
 hrGluAlaValGlnLysValSerThrGluSerIleValIleTrpGlyLysIleProLys 543 L
 CAGAGGCAGTGCAAAAGTATCCACAGAAAGCATAGTAATATGGGAAAGATTCCCTAAAT

FIG. 5C

REPLACEMENT SHEET

PheLysLeuProIleGlnLysGluThrTrpGluAlaTrpTrpMetGluTyrTrpGlnAlaT
 3268 TAAACTACCCATACAAAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCTA
 hrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGln 583
 CCTGGATTCCCTGAGTGGGAGTTGTCAATACCCCTCCCTAGTGAAATTATGGTACCACT
 LeuGluLysGluProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArgG
 3388 TAGAGAAAGAACCCATAGTAGGAGCAGAAACTTCTATGTAGATGGGCAGCTAATAGGG
 IuThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSer 623
 AGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAGTTGTCTCCA
 IleAlaAspThrThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAspS
 3508 TAGCTGACACAACAAATCAGAAGACTGAATTACAAGCAATTCTAGCTTGCAGGATT
 erGlyLeuGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAla 663
 CGGGATTAGAAGTAAACATAGTAACAGACTCACAAATATGCATTAGGAATCATTCAAGCAC
 GlnProAspLysSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLysLysG
 3628 AACCAGATAAGAGTGAATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAGG
 lLysValTyrLeuAlaTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnVal 703
 AAAAGGTCTACCTGGCATGGTACAGCACACAAAGGAATTGGAGGAAATGAACAGTAG
 AspLysLeuValSerAlaGlyIleArgLysValLeuPheLeuAsnGlyIleAspLysAlaG
 3748 ATAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTGAATGGAATAGATAAGGCC
 InGluGluHisGluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeu 743
 AAGAAGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTAACCTGC
 ProProValValAlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGluA
 3868 CACCTGTAGTAGCAAAGAAATAGTAGCCAGCTGTGATAATGTCAGCTAAAGGAGAAG
 laMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeu 783
 CCATGCATGGACAAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAG
 GluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIleGluAlaGluValI
 3988 AAGGAAAAATTATCCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAACAGAAGTTA
 leProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeuAlaGlyArgTrp 823
 TTCCAGCAGAGACAGGGCAGGAAACAGCATATTTCTTAAATTAGCAGGAAGATGGC
 ProValLysThrIleHisThrAspAsnGlySerAsnPheThrSerThrThrValLysAlaA
 4108 CAGTAAAAACAATACATACAGACAATGGCAGCAATTTCACCAGTACTACGGTTAAGGCCG
 IaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGln 863
 CCTGTTGGTGGGCAGGGATCAAGCAGGAATTGGCATTCCCTACAATCCCCAAAGTCAG
 GlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGlnA
 4228 GAGTAGTAGAATCTATGAATAATGAATTAAAGAAAATTAGGACAGGTAAAGAGATCAGG
 IaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLys 903
 CTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCCACAATTAAAAGAAAAG
 GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIleG
 4348 GGGGGATTGGGGGATACAGTGCAGGGAAAGAAATAGTAGACATAATAGCAACAGACATAC
 InThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArg 943
 AACTAAAGAACTACAAAAGCAAATTACAAAATTCAAAATTTCGGTTTATTACAGGG

FIG. 5D

REPLACEMENT SHEET

AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAlaV
 4468 ACAACAAAGATCCCTTGGAAAGGACCAGCAAAGCTCTGGAAAGGTGAAGGGGCAG
 a1ValIleGlnAspAsnSerAspIleLysValValProArgArgLysAlaLysIleIle 983
 TAGTAATAACAAGATAATAGTGACATAAAAGTAGTGCCAGAAGAAAAGCAAAAATCATTA
 ArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArgGlnAspGluAspA
 4588 GGGATTATGGAAAACAGATGGCAGGTGATGATTGTGGCAAGTAGACAGGATGAGGATT
 M
 AGAACATGGAAAAGTTAGTAAAACACCATAATGTATATTCAAAGAAAGCTAAAGGATGG
 4708 TTTTATAGACATCACTATGAAAGTACTCATCCAAGAGTAAGTTCAAAGTACACATCCCC
 CTAGGGGATGCTAAATTGTAATAACAACATATTGGGTCTGCATAACAGGAGAAAGAGAA
 4828 TGGCATTGGGCCAGGGAGTCGCCATAGAATGGAGGAAAAGAAATATAGCACACAAGTA
 GACCCTGGCTAGCAGACCAACTAATTCTGCATTATTTGATTGTTTCAGAATCT
 4948 GCTATAAAAATGCCATATTAGGATATAGAGTTAGTCTAGGTGTGAATATCAAGCAGGA
 CATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTATAACACCAAAAAAG
 5068 ACAAAAGCCACCTTGCCTAGTGTAAAGAAACTGACAGAGGATAGATGGAACAAGCCCCAG
 AAGACCAAGGGCCACAGAGGGAGCCATAATGAATGGACACTAGAGCTTTAGAGGAGC
 5188 TTAAGAGAGAAGCTGTTAGACATTTCCTAGGCCATGGCTCCATAGCTTAGGACAATATA
 TCTATGAAACTTATGGGGATACTTGGCAGGAGTGGAAAGCCATAATAAGAATTCTGCAAC
 5308 AACTGCTGTTATTCAATTCAAAGATTGGGTGTCAACATAGCAGAAATAGGCATTATTCAAC
 AGAGGAGAGCAAGAAGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCATTCA
 5428 GGAAGTCAGCCTAGGACTGCTGTAACAATTGCTATTGTAAGGAAAGTGTGCTTCATTGC
 TACCGTGTTCACAAGAAAAGGCTAGGCATCTCTATGGCAGGAAGAAGCGGAGACAG
 5548 CGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTCTATCAAAGCAGTAAGTA
 GTAAATGTAATGCAATCTTACAATATTAGCAATAGTATCATTAGTAGTAGTGTAGCAATA
 5668 ATAGCAATAGTTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAAAGA
 MetLysVal 3
 AAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAAGTG
 LysGlyThrArgArgAsnTyrGlnHisLeuTrpArgTrpGlyThrLeuLeuLeuGlyMet
 5788 AAGGGGACCAGGAGGAATTATCAGCACTTGTGGAGATGGGGCACCTGCTCCTGGGATG
 LeuMetIleCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValProVal
 TTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTACAGTTATTATGGAGTACCTGTG 43
 TrpLysGluAlaThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThrGlu
 5908 TGAAAAGAAGCAACTACCACTCTATTTGTGCATCAGATGCTAGAGCATATGATAACAGAG
 ValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGluVal
 GTACATAATGTTGGGCCACACATGCCTGTGACCCACAGACCCCCAACCCACAAGAAGTA 83

FIG. 5E

REPLACEMENT SHEET

6028 ValLeuGlyAsnValThrGluAsnPheAsnMetTrpLysAsnAsnMetValGluGlnMet
 GTATTGGGAAATGTGACAGAAAATTTAACATGTGGAAAAATAACATGGTAGAACAGATG
 GlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThrPro 123
 CAGGAGGATATAATCAGTTATGGGATCAAAGCTAACGCCATGTGTAAAATTAAACCCCA
 LeuCysValThrLeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSerAsn
 6148 CTCTGTGTTACTTAAATTGCACTGATTGGGGAAAGGCTACTAACATACCAATAGTAGTAAT
 TrpLysGluGluIleLysGlyGluIleLysAsnCysSerPheAsnIleThrThrSerIle 163
 TGGAAAGAAGAAATAAAAGGAGAAATAAAAAACTGCTCTTCATATCACCAACAAGCATA
 ArgAspLysIleGlnLysGluAsnAlaLeuPheArgAsnLeuAspValValProIleAsp
 6268 AGAGATAAGATTCAAGAAAGAAAATGCACCTTCGTAAACCTTGATGTAGTACCAATAGAT
 AsnAlaSerThrThrAsnTyrThrAsnTyrArgLeuIleHisCysAsnArgSerVal 203
 AATGCTAGTACTACTACCAACTATACCAACTATAGGTTGATACATTGTAACAGATCAGTC
 IleThrGlnAlaCysProLysValSerPheGluProIleProIleHisTyrCysThrPro
 6388 ATTACACAGGCCTGTCAAAGGTATCATTTGAGCCAATTCCCACATACATTATTGTACCCCG
 AlaGlyPheAlaIleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCysThr 243 E
 GCTGGTTTGCATTCTAAAGTGTAAATAATAAACGTTCAATGGAAAAGGACCATGTACA
 AsnValSerThrValGlnCysThrHisGlyIleArgProIleValSerThrGlnLeuLeu
 6508 AATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTGCTG
 LeuAsnGlySerLeuAlaGluGluGluValValIleArgSerAspAsnPheThrAsnAsn 283 N
 TTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTACGAACAAT
 AlaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgProAsn
 6628 GCTAAAACCATAATAGTACAGCTGAATCTGTAGCAATTAACTGTACAAGACCCAC
 AsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAlaPheHisThrThrGlyArg 323 V
 AACAAATAAGAAAAAGTATCTATAGGACCAGGGAGAGCATTCAACACAGGAAGA
 IleIleGlyAspIleArgLysAlaHisCysAsnIleSerArgAlaGlnTrpAsnAsnThr
 6748 ATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGAGCACAAATGGAATAACACT
 LeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsnAsnLysThrIleValPhe 363
 TTAGAACAGATAGTTAAAAATTAAAGAGAACAGTTGGGATAATAAAACAATAGTCTT
 AsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGlyGlu
 6868 AATCAATCCTCAGGAGGGACCCAGAAATTGTAATGCACAGTTAAATTGTAGAGGGGAA
 PhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThrGlu 403
 TTTTCTACTGTAATACAACACAACGTTAAATAATACATGGAGGTAAATCACACTGAA
 GlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsnMet
 6988 GGAACTAAAGGAAATGACACAATCATACTCCCATGTAAGATAAAACAAATTATAAACATG
 TrpGlnGluValGlyLysAlaMetTyrAlaProProIleGlyGlyGlnIleSerCysSer 443
 TGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCATTGGAGGACAAATTAGTTGTTCA
 SerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAspThr
 7108 TCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTACAAATGTAACATAATGACACC
 GluValPheArgProGlyGlyGlyAspMetArgAspAsnTrpArgSerGluLeuTyrLys 483
 GAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATAAAA

FIG. 5F

REPLACEMENT SHEET

7228 TyrLysValIleLysIleGluProLeuGlyIleAlaProThrLysAlaLysArgArgVal
 TATAAAGTAATAAAAATTGAACCATTAGGAATAGCACCCACCAAGGCAAAGAGAAAGAGTG
 ValGlnArgGluLysArgAlaValGlyIleValGlyAlaMetPheLeuGlyPheLeuGly 523
 GTGCAGAGAGAAAAAGAGCAGTGGGAATAGTAGGAGCTATGTTCCCTGGGTTCTGGGA
 AlaAlaGlySerThrMetGlyAlaValSerLeuThrLeuThrValGlnAlaArgGlnLeu
 GCAGCAGGAAGCACTATGGGCGCAGTGTCAATTGACGCTGACGGTACAGGCCAGACAATT
 LeuSerGlyIleValGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGlnHis 563
 TTGTCTGGTATAGTGCACAGCAGAACATTGCTGAGGGCTATTGAGGCGAACAAACAT
 LeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaValGly
 7468 CTGTTGCAACTCACAGCTGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAA
 ArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIleCys 603
 AGATACCTAACGGATCAACAGCTCTAGGGATTGGGTTGCTCTGGAAAACATTTGC
 ThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrpAsp
 7588 ACCACTGCTGTGCCTTGGATGCTAGTTGGAGTAATAATCTCTGGAAAGACATTGGGAT
 AsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyrThr 643
 AACATGACCTGGATGCAGTGGAAAGAGAAATTGACAATTACACAAACACAATACACC
 LeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeuAsp
 7708 TTACTTGAAAGATCGCAGAACACAAGAAAAGAATGAACAAGAATTATTAGAATTGGAT
 LysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpLeuTrpTyrIleLysIle 683
 AAGTGGGCAAGTTGTGGATTGGTTAGCATAACAAACTGGCTGTGGTATATAAGATA
 PheIleMetIleValGlyGlyLeuValGlyLeuArgIleValPheAlaValLeuSerIle E
 7828 TTCATAATGATAGTAGGAGGCTTGGTAGGTTAAGAATAGTTTGCTGTGCTTCTATA
 ValAsnArgValArgGlnGlyTyrSerProLeuSerPheGlnThrArgLeuProValPro 723
 GTGAATAGAGTTAGGCAGGGATACTCACCATGTCATTGACAGCCCCCTCCAGTCCCG N
 ArgGlyProAspArgProAspGlyIleGluGluGluGlyGluArgAspArgAspArg
 7948 AGGGGACCCGACAGGCCGACGGAAATCGAAGAAGGTGGAGAGAGACAGAGACAGA
 SerValArgLeuValAspGlyPheLeuAlaLeuIleTrpGluAspLeuArgSerLeuCys 763 V
 TCCGTTGATTAGTGGATGGATTCTTAGCATTCTGGGAAGATCTGCGGAGCCTGTGC
 LeuPheSerTyrArgArgLeuArgAspLeuLeuIleAlaAlaArgThrValGluIle
 8068 CTCTTCAGCTACCGCCGCTTGGAGAGACTTACTCTGATTGCTGAGCGAGGACTGTGGAAATT
 LeuGlyHisArgGlyTrpGluAlaLeuLysTyrTrpTrpSerLeuLeuGlnTyrTrpIle 803
 CTGGGGCACAGGGGGTGGAAAGCCCTCAAATATTGGTGGAGTCTCCTGCAGTATTGGATT
 GlnGluLeuLysAsnSerAlaValSerTrpLeuAsnAlaThrAlaIleAlaValThrGlu
 8188 CAGGAACTAAAGAATAGTGCTTAGCTGGCTAACGCCACAGCTATAGCAGTAACGAG
 GlyThrAspArgValIleGluValAlaGlnArgAlaTyrArgAlaIleLeuHisIleHis 843
 GGGACAGATAGGGTTATAGAAGTAGCACAAGAGCTTATAGAGCTATTCTCACATACAT
 ArgArgIleArgGlnGlyLeuGluArgLeuLeuLeuOC
 8308 AGAAGAATTAGACAGGGCTTGGAAAGGCTTTGCTATAAGATGGGTGGCAAGTGGTCAA
 ACGTAGTATGGGTGGATGGTCTGCTATAAGGAAAGAATGAGACGAGCTGAGCCACGAGC

FIG. 5G

REPLACEMENT SHEET

8428 TGAGCCAGCAGCAGATGGGTGGGAGCAGTATCTCGAGACCTGGAAAAACATGGAGCAAT
CACAAGTAGCAATACAGCAGCTACTAATGCTGATTGTGCCTGGCTAGAACAGACAAGAGGA
8548 GGAAGAGGTGGGTTTCAGTCAGACCTCAGGTACCTTAAGACCAATGACTTACAAGGC

AGCTTAGATATTAGCCACTTTAAAAGAAAAGGGGGGA ^{U3}→ CTGGAAGGGCTAATTGGT

8667 CCCAAAGAACAGAGATCCTTGATCTGGATCTACACACACACAGGCTACTTCCCTG
ATTGGCAGAATTACACACCAGGCCAGGGATCAGATATCCACTGACCTTGGATGGTGC

8787 TCAAGCTAGTACCAAGTTGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGAACACA
GCTTGTACACCTATGAGCCTGCATGGATGGAGGACGCCAGAAAGAAGTGTAGTGT

8907 GGAGGTTGACAGCAAACTAGCATTCATCACATGGCCGAGAGCTGCATCCGGAGTACT
ACAAAGACTGCTGACATCGAGCTTCTACAAGGGACTTCCGCTGGGACTTCCAGGGA

9027 GGCCTGGCCTGGCGGGACTGGGAGTGGCGTCCCTCAGATGCTGCATATAAGCAGCTGC

TTTTGCCTGTACTG ^{← U3 R →} GGTCTCTGGTTAGACCAGATCTGAGCCTGGAGCTCTGGC

9146 TAACTAGGGAACCCACTGCTTAAGCCTCAATAAGCTTGCCTGAGTGCTTCA AGTAGT
GTGTGCCGTCTGTTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTAGTCAGT

9265 GTGGAAAAATCTCTAGCAG ^{← U5}

L

T

R

FIG. 5H

REPLACEMENT SHEET

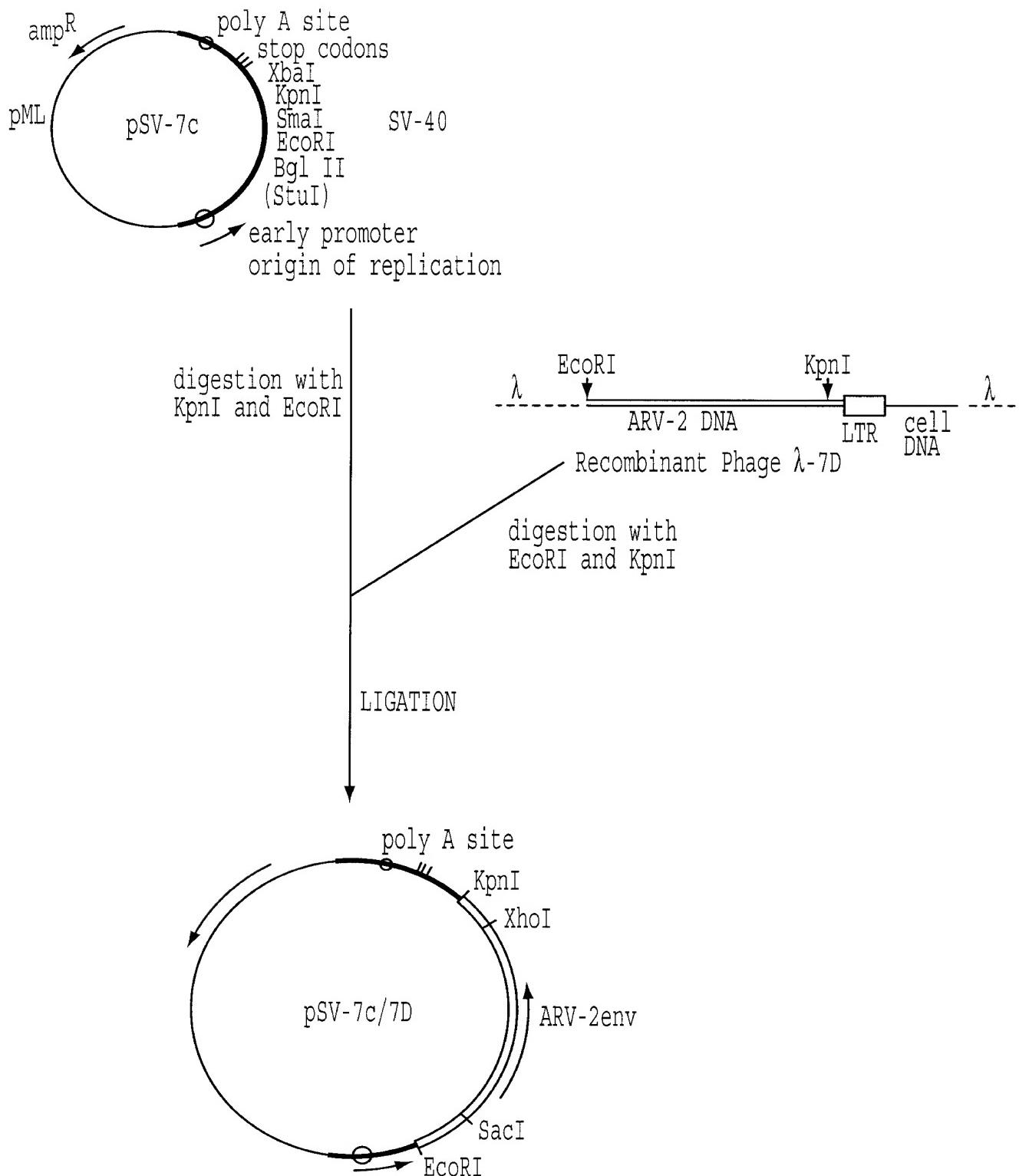


FIG. 6

REPLACEMENT SHEET

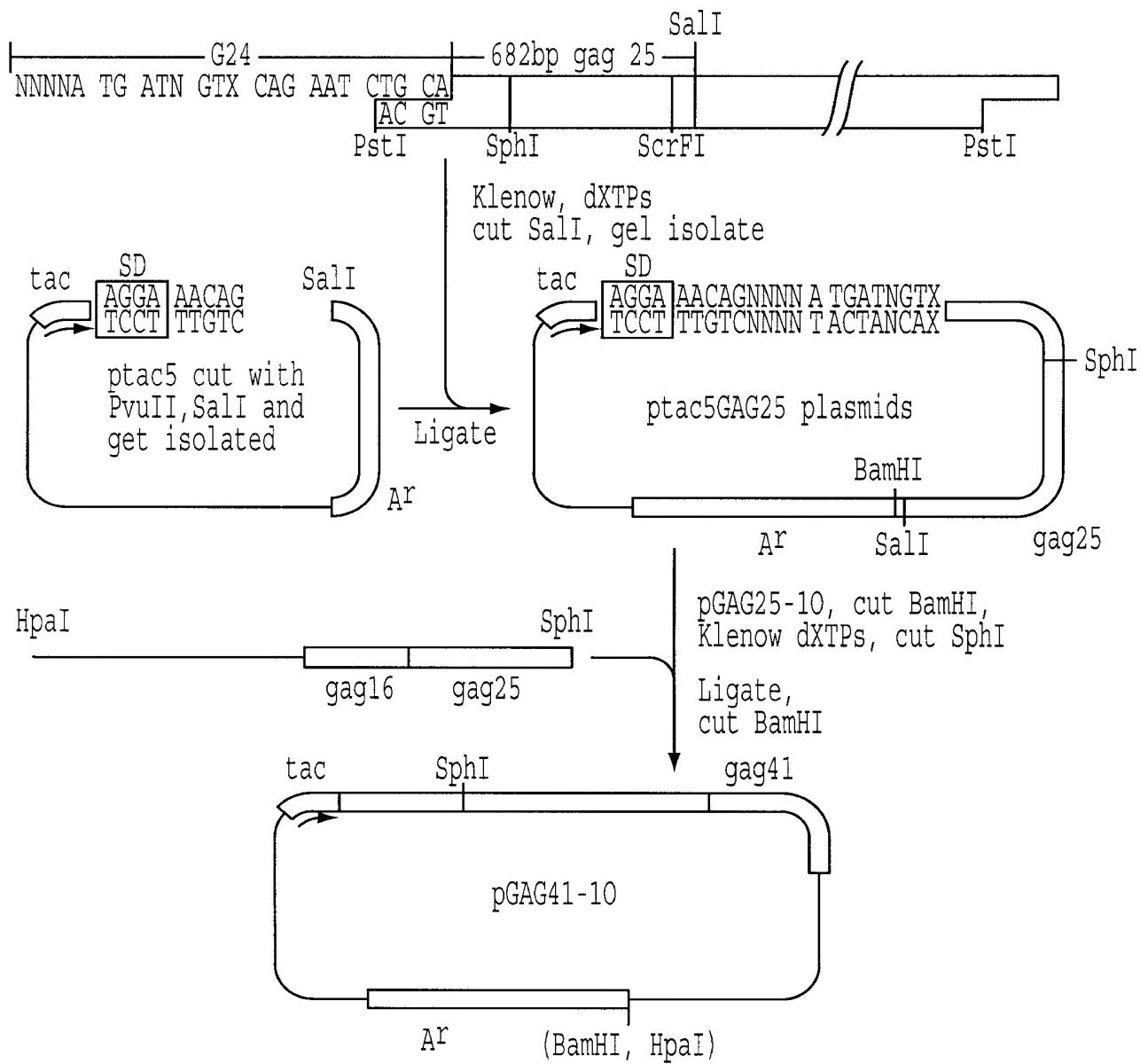


FIG. 7

REPLACEMENT SHEET

ptac 5 Promotor	Met Ile Val ATG ATCGTA
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* * *

748 GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
CAGAACATCTGCAGGGCAAAATGGTACATCAGGCCATATCACCTAGAACATTAAATGCATGG

181 ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
GTAAAAGTAGTAGAAGAAAAGGCTTCAGCCCAGAAGTAATAACCATGTTTCAGCATTAA

868 SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
TCAGAAGGAGCCACCCCACAAGATTAAACACCATGCTAAACACAGTGCCCCACATCAA

221 AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal
GCAGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATAGAGTG

988 HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp
CATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGGGGAAGTGAC

261 IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro
ATAGCAGGAACTACTAGTACCCCTTCAGGAACAAATAGGATGGATGACAAATAATCCACCT

1108 IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg
ATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGA

301 MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp
ATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAGGAACCCCTTAGAGAT

1228 TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn
TATGTAGACCGGTTCTATAAAACTCTAACAGAGCCGAACAAGCCTCACAGGATGTAAGACT

341 TrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys
TGGATGACAGAACCTTGTGGTCCAAATGCAAACCCAGATTGTAAGACTATTTAAAAA

1348 AlaLeuGlyProAlaAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGly
GCATTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGGGA

ProGlyHisLysAlaArgValLeu Stop Stop
CCCGGGCATAAAGCAAGAGTTTGTGATAG

ptac 5	
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FIG. 8

REPLACEMENT SHEET

	ptac 5 Promotor	MetIleVal 141 ATGATCGTA
--	-----------------	----------------------------

748 GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
CAGAACTGCAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACCTTAAATGCATGG
 ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu 181
GTAAAAGTAGTAGAAGAAAAGGCTTCAGCCCAGAAGTAATAACCATGTTTCAGCATTAG
 SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln 868
TCAGAAGGAGCCACCCACAAGATTAAACACCATGCTAACACACAGTGGGGGACATCAA
 AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal 221
GCAGGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAACATGGATAGAGTG
 HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp 988
CATCCAGTGCATGCAGGGCTATTGCACCAGGCCAAATGAGAGAACCAAGGGGAAGTGAC A
 IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro 261
ATAGCAGGAACTACTAGTACCCCTCAGGAACAAATAGGATGGATGACAAATAATCCACCT
 IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg 1108
ATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGATTAAATAAAATAGTAAGA G
 MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp 301
ATGTATAGCCCTACCAAGCATTCTGGACATAAGACAAGGCCAAAGGAACCCCTTAGAGAT
 TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn 1228
TATGTAGACCAGGTTCTATAAAACTCTAAGAGCGAACAGCTTCACAGGATGTAAGGAA
 TrpMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys 341
TGGATGACAGAACCTTGGTCCAAATGCAAACCCAGATTGTAAGACTATTTAAAAA
 AlaLeuGlyProAlaAlaAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGly 1348
GCATTGGGACCAGCAGCTACACTAGAAAGAAATGATGACAGCATGTCAGGGAGTGGGGGA
 ProGlyHisLysAlaArgValLeuAlaGluAlaMetSerGlnValThrAsnProAlaAsn 381
CCCAGGCCATAAAGCAAGAGTTTGGCTGAAGCCATGAGCCAAGTAACAAATCCAGCTAAC
 IleMetMetGlnArgGlyAsnPheArgAsnGlnArgLysThrValLysCysPheAsnCys 1468
ATAATGATGCAGAGAGGCAATTAGGAACCAAAGAAAGACTGTTAAGTGTTCATTG
 GlyLysGluGlyHisIleAlaLysAsnCysArgAlaProArgLysGlyCysTrpArg 421
GGCAAAGAACGGCACATAGCCAAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAGA
 CysGlyArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGly 1588
TGTGGAAGGGAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTAGGG
 LysIleTrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluPro 461
 luAspLeuAlaPheLeuGlnGlyLysAlaArgGluPheSerSerGluGlnThrArgAla 23
AAGATCTGGCCTTCCTACAAGGGAGGCCAGGGAAATTCTCAGAGCAGACCAGAGCCA
 ThrAlaProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLys 1708
 AsnSerProThrArgArgGluLeuGlnValTrpGlyGlyGluAsnAsnSerLeuSerGluA
ACAGCCCCACCAGAACAGAGCTTCAGGTTGGGGAGGAGAAAACAACCTCCCTCTCAGAAC
 GlnGluProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsn 501
 laGlyAlaAspArgGlnGlyThrValSerPheAsnPheProGlnIleThrLeuTrpGln 63
CAGGAGCCGATAGACAAGGAACTGTATCCTTAACCTCCCTCAGATCACTCTTGGCAAC

FIG. 9A

REPLACEMENT SHEET

AspProSerSerGlnOC
 ArgProLeuValThrIleArgIleGlyGlyGlnLeuLysGluAlaLeuLeuAspThrGlyA
 1828 GACCCCTCGTCACAATAAGGATAGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAG

 IaAspAspThrValLeuGluGluMetAsnLeuProGlyLysTrpLysProLysMetIle 103
 CAGATGATACTAGTATTAGAAGAAAATGAATTGCCAGGAAATGGAAACCAAAATGATAG

 GlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGlnIleProValGluIleCysG
 1948 GGGGAATTGGAGGTCTTATCAAAGTAAGACAGTACGATACCTGTAGAAATCTGTG
 lyHisLysAlaIleGlyThrValLeuValGlyProThrProValAsnIleIleGlyArg 143
 GACATAAACGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAA

 AsnLeuLeuThrGlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrValP
 2068 ATCTGTTGACTCAGATTGGTTGACTTTAAATTCCCCATTAGTCCTATTGAAACTGTAC
 roValLysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeuThrGlu 183
 CAGTAAATTAAAGCCAGGAATGGATGGCCAAAAGTTAAGCAATGCCATTGACAGAAG

 GluLysIleLysAlaLeuValGluIleCysThrGluMetGluLysGluGlyLysIleSerL
 2188 AAAAATAAAAGCATTAGTAGAGATATGTACAGAAATGGAAAAGGAAGGGAAAATTCAA
 ysIleGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSer 223
 AAATTGGGCCTGAAAATCCATACAATACTCCAGTATTGCTATAAGAAAAAGACAGTA

 ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrpG
 2308 CTTAAATGGAGAAAATAGTAGATTTCAGAGAACTTAATAAAAGAACTCAAGACTCTGGG
 luValGlnLeuGlyIleProHisProAlaGlyLeuLysLysLysSerValThrVal 263
 AAGTTAGTTAGGAATACCACACCCCGCAGGGTTAAAAAGAAAAATCAGTAACAGTAT

 LeuAspValGlyAspAlaTyrPheSerValProLeuAspLysAspPheArgLysTyrThrA
 2428 TGGATGTGGGTATGCATACTTTAGTTCCCTAGATAAGACTTTAGAAAGTATACTG
 IaPheThrIleProSerIleAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnVal 303
 CATTACCATACCTAGTATAACAAATGAGACACCAGGGATTAGATATCAGTACAATGTGC

 LeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeuG
 2548 TGCCACAGGGATGGAAAGGATCACCAAGCAATATTCAAAGTAGCATGACAAAAATCTTAG
 luProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr 343
 AGCCTTTAGAAAACAGAATCCAGACATAGTTATCTATCAATACATGGATGATTGTATG

 ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHisL
 2668 TAGGATCTGACTTAGAAATAGGGCAGCATAAGAACAAAAATAGAGGAACGTGAGACAGCATC
 euLeuArgTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeu 383
 TGTTGAGGTGGGGATTACCAACACCAGACAAAAACATCAGAAAGAACCTCCATTCTTT

 TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGluL
 2788 GGATGGGTTATGAACTCCATCCTGATAATGGACAGTACAGCCTATAATGCTGCCAGAAA
 ysAspSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer 423
 AAGACAGCTGGACTGTCAATGACATAAGAAGTTAGTGGAAAATTGAATTGGCAAGTC

 GlnIleTyrAlaGlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyThrLysAlaL
 2908 AGATTATGCAGGGATTAAAGTAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCAC
 euThrGluValIleProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGlu 463 P
 TAACAGAAGTAATACCACTAACAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAGA O
 L

FIG. 9B

REPLACEMENT SHEET

IleLeuLysGluProValHisGluValTyrTyrAspProSerLysAspLeuValAlaGluI
3028 TTCTAAAAGAACCAAGTACATGAAGTATATTATGACCCATCAAAGACTTAGTAGCAGAAA
IeGlnLysGlnGlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsn 503
TACAGAACGCAGGGGCAAGGCCAATGGACATATCAAATTATCAAGAGCCATTAAAAATC
LeuLysThrGlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeuT
3148 TGAAACAGGAAAGTATGCAAGGATGAGGGGTGCCACACTAATGATGTAAAACAGTT
hrGluAlaValGluLysValSerThrGluSerIleValIleTrpGlyLysIleProLys 543
ptac 5

FIG. 9C

REPLACEMENT SHEET

ARV GAG p16 - synthetic Parts A and B

5' arv 234 3'
 MetGlnArgGlyAsnPheArgAsnGlnArgLysThrValLysCysPheAsnCysGlyLys
 TATTATGCAAAGAGGTAACTTCAGGAATCAAAGAAAGACCGTTAAGTGGTCAACTGTGGTAAG
 ATAATACGTTCTCCATTGAAGTCCTTAGTTCTTCTGGCAATTACAAAGTTGACACCATTC
 3' ^ arv 235 5'
 10 mn11, 23 hinfl,

 63 GluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysAlaCysTrpArgCysGly
 GAAGGTACATCGCTAAGAACTGTAGAGCTCAAGAAAAGAAGGCTTGGAGATGTGGT
 CTTCCAGTGTAGCGATTCTGACATCTCGAGGTTCTTCCGAACAAACCTCTACACCA
 76 dde1, 88 ban2 hgiA hgiJ11 sac1 sdul, 89 alu1,

 123 ArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIle
 AGAGAAAGGTACCAAATGAAGGACTGTACCGAAAGACAAGCTAACCTCTGGGTAAGATC
 TCTCTTCCAGTGGTTACTTCCTGACATGGCTTCTGTTGATTGAAGAACCCATTCTAG
 129 bstE2, 131 hph, 148 rsal, 161 alu1, 178 bgl11 xho2, 179
 sau3a,

 183 TrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAla
 TGGCCATCTTACAAGGGTAGACCAGGTAACTCTTGCAATCCAGACCAGAACCAACCGCT
 ACCGGTAGAATGTTCCCCTGGTCCATTGAAGAACGTTAGGTCTGGTCTGGTTGGCGA
 183 bal1 cfr1 hael, 184 hael11, 199 accl, 204 apyl ecor11 sc
 rF1,

 243 ProProGluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLysGlnGlu
 CCACCTGAAGAAAGTTCAAGGTTGGTGAAGAAAAGACCACCCATCTCAAAAGCAAGAA
 GGTGGA~~C~~TTCTTCAAAGCCAAGCCACTTCTTTCTGGTGGGGTAGAGTTTCGTTCT
 249 mbol1, 267 hph, 270 mbol1,

 303 ProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsnAspPro
 CCAATCGACAAGGAATTGTACCCATTGACCTTTGAGATCCTTGGTAACGATCCC
 GGTTAGCTGTTCTTAACATGGGTAACTGGAGAAACTCTAGGAACAAGCCATTGCTAGGG
 307 taq1, 320 rsal, 331 mn11, 339 xho2, 340 sau3a, 357 sau3a,
 361 mn11, 362 aval xhol,

 363 SerSerGlnOP AM
 TCGAGGCCAATGATAG
 AG~~C~~TCGGTTACTATCAGCT
 363 taq1, 377 accl hind11 sal1

FIG. 10

REPLACEMENT SHEET

PYK Promoter	<u>MetSer</u> <u>ATGTCT</u>
ArgIleAspCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValProVal 51	
<u>AGAACATCGAT</u> GTAGTGCTACAGAAAAATTGTGGGTACAGTTATTATGGAGTACCTGTG	
TrpLysGluAlaThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThrGlu 5908	
5908 TGGAAAGAAGCAACTACCACTCTATTGTGCATCAGATGCTAGAGCATATGATAAGAG	
ValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGluVal 91	
GTACATAATGTTGGGCCACACATGCCTGTGTACCCACAGACCCCCAACCCACAAGAAGTA	
ValLeuGlyAsnValThrGluAsnPheAsnMetTrpLysAsnAsnMetValGluGlnMet 6028	
6028 GTATTGGAAATGTGACAGAAAATTAAACATGTGGAAAAATAACATGGTAGAACAGATG	
GlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThrPro 131	
CAGGAGGGATAATACTAGTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAAACCCA	
LeuCysValThrLeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSerAsn 6148	
6148 CTCTGTGTTACTTTAAATTGCACTGATTGGGAAGGCTACTAATACCAATAGTAGTAAT	
TrpLysGluGluIleLysGlyGluIleLysAsnCysSerPheAsnIleThrThrSerIle 171	
TGGAAAGAAGAAATAAAAGGAGAAATAAAAAGTCTTTCAATATCACCAAGCATA	
ArgAspLysIleGlnLysGluAsnAlaLeuPheArgAsnLeuAspValValProIleAsp 6268	
6268 AGAGATAAGATTCAAGAAAGAAATGCACTTTTCGTAAACCTTGATGTAGTACCAATAGAT	
AsnAlaSerThrThrAsnTyrThrAsnTyrArgLeuIleHisCysAsnArgSerVal 211	
AATGCTAGTACTACTACCAACTATACCAACTATAGGTTGATACATTGTAACAGATCAGTC	
IleThrGlnAlaCysProLysValSerPheGluProIleProIleHisTyrCysThrPro 6388	
6388 ATTACACAGGCCGTGCCAAAGGTATCATTGAGCCAATTCCCACACATTGTACCCCG	
AlaGlyPheAlaIleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCysThr 251	
GCTGGTTTGCATTCTAAAGTGTAAATAAAACGTTCAATGGAAAAGGACCATGTACA	

FIG. 11A

REPLACEMENT SHEET

6508 AsnValSerThrValGlnCysThrHisGlyIleArgProIleValSerThrGlnLeuLeu
 AATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTGCTG
 LeuAsnGlySerLeuAlaGluGluGluValValIleArgSerAspAsnPheThrAsnAsn 291
 TTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACGAACAAT
 AlaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgProAsn
 GCTAAAACCATAATAGTACAGCTGAATCTGTAGCAATTAACTGTACAAGACCCAAC
 AsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAlaPheHisThrThrGlyArg 331
 ACAACATACAAGAAAAAGTATCTATATAGGACCAGGGAGAGCATTCTACAAACAGGAAGA
 IleIleGlyAspIleArgLysAlaHisCysAsnIleSerArgAlaGlnTrpAsnAsnThr
 ATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGAGCACAATGGAATAACACT
 LeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsnAsnLysThrIleValPhe 371
 TTAGAACAGATAGTTAAAAAATTAAGAGAACAGTTGGAAATAATAAAACAATAGTCTT
 AsnGlnSerSerGlyGlyAspProGluIleValMetHisSerPheAsnCysArgGlyGlu
 6868 AATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTAATTGTAGAGGGAA 411 E
 PhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThrGlu
 TTTTCTACTGTAATACAACACAATGTTAATAATACATGGAGGTTAAATCACACTGAA
 GlyThrLysGlyAsnAspThrIleIleLeuProCysArgIleLysGlnIleIleAsnMet
 6988 GGAACATAAGGAAATGACACAATCATACTCCCAGTGAGAATAAAACAAATTATAAACATG N
 TrpGlnGluValGlyLysAlaMetTyrAlaProProIleGlyGlyGlnIleSerCysSer
 TGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCATTGGAGGACAAATTAGTTGTTCA
 SerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAspThr
 7108 TCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTACAAATGTAACATGACACC V
 GluValPheArgProGlyGlyGlyAspMetArgAspAsnTrpArgSerGluLeuTyrLys 491
 GAGGTCTTCAGACCTGGAGGAGGAGATGAGGGACAATTGGAGAAGTGAATTATATAAA
 TyrLysValIleLysIleGluProAsnSerValSer
 7228 TATAAAGTAATAAAATTGAACCAATTCGGTATCTTGA PYK Terminator

FIG. 11B

REPLACEMENT SHEET

Nucleotide positions relative to Figure 5.	Met Ile Asp Lys Ala Gln Glu Glu His Glu Lys Tyr His Ser Asn Trp
	1 AGGXAACAG:::ATGAT:GA:AAAGGCACAAGAAGAACATGAGAAATATCACAGTAATTGG TCCXTTGTGTC:::TACTA:CT:TTCCGTGTTCTCTTGACTCTTATAGTGTCAATTAACC
	32 mbo11, 38 nial11,
3820	Arg Ala Met Ala Ser Asp Phe Asn Leu Pro Pro Val Val Ala Lys Glu Ile Val Ala Ser 62 AGAGCCATGGCTAGTGATTTAACCTGCCACCTGTAGTAGCAAAGAAAATAGTAGGCCAGC TCTCGGTACCGATCACTAAAATTGGACGGTGGACATCATGTTTCTTATCATCGGTGCG 66 ncol, 67 nial11, 118 nspBII pnull, 119 alu1,
3880	Cys Asp Lys Cys Gln Leu Lys Gly Glu Ala Met His Gly Gln Val Asp Cys Ser Pro Gly 122 TGTGATAAAATGTCAGCTAAAGAGAAGCAGTCATGGACAAAGTAGACTGTAGTCCAGGA ACACTATTTACAGTCGATTTCTCTCGGTACGTACCTGTTCATCTGACATCAGGTCCT 135 alu1, 151 nial11, 152 nsil ava3, 155 nial11, 164 accl, 1 76 apyl bstXI ecor11 scrF1,
3940	Ile Trp Gln Leu Asp Cys Thr His Leu Glu Gly Lys Ile Ile Leu Val Ala Val His Val 182 ATATGGCAACTAGATTGTACACATCTAGAAAGGAAAAATTATCCTGGTAGCAGGTCATGTA TATACCGTTGATCTAACATGTGTAGATCTCCTTTAAAGGACCATCGTCAGTACAT 198 rsal, 205 xba1, 223 apyl ecor11 scrF1, 236 nial11,
4000	Ala Ser Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr 242 GCCAGTGGATATATAGAACGAGAAGTTATTCAGCAGAGACAGGGCAGGAAACAGCATAT CGGTACCTATATATCTCGTCTTCATAAGGTCGTCTGTCCCCGTCCTTGTGTTATA 263 xmn1,
4060	Phe Leu Leu Lys Leu Ala Gly Arg Trp Pro Val Lys Thr Ile His Thr Asp Asn Gly Ser 302 TTTCTCTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAAATGGCAGC AAAGAGAATTAACTCGTCCTCTACCGGTCTTTGTTATGTATGTTACCGTCG 321 mbo11, 326 ball cfr1 hael, 327 hael11, 357 bbv fnu4h1,
4120	Asn Phe Thr Ser Thr Thr Val Lys Ala Ala Cys Trp Trp Ala Gly Ile Lys Gln Glu Phe 362 AATTCACCAAGTACTACGGTTAAGGCCGCTGTTGGGGCAGGGATCAAGCAGGAATT TTAAAGTGGTCAATGCCAATTCCGGCGGACAACCACCCGTCCAGTTCGTCCTTAA 366 hph, 371 scal, 372 rsal, 385 hael11, 386 fnu4h1 nsbl1, 4 05 bin1, 406 dpn1 sau3a,
4180	Gly Ile Pro Tyr Asn Pro Gln Ser Gln Gly Val Val Glu Ser Met Asn Asn Glu Leu Lys 422 GGCATTCCCTACAATCCCCAAAGTCAGGAGTAGTGAATCTATGAATAATGAATTAAAG CCGTAAGGGATGTTAGGGGTTTCAGTTCTCATCTTAGATAACTTATTACTTAATTTC 423 bsm1, 458 hinf1,
4240	Lys Ile Ile Gly Gln Val Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gln Met Ala 482 AAAATTATAGGACAGGTAAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCA TTTTAATATCCTGTCATTCTAGTCGACTTGTGGAAATTCTGTCGTATGTTACCGT 503 dpn1 sau3a, 518 af111, 530 rsal,
4300	Val Phe Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser Ala Gly Glu Arg 542 GTATTCACTCCACAATTAAAAGAAAAGGGGGATTGGGGGATACAGTGCAGGGGAAAGA CATAGTAGGTGTTAAATTTCTTCCCCCTAACCCCCCTATGTCACGTCCCCTTCT 547 fok1, 557 ahall1,

FIG. 12A

REPLACEMENT SHEET

4360	IleValAspIleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLys
	602 ATAGTAGACATAATAGCAACAGACATACAAACTAAAGAACTACAAAAGCAAATTACAAAAA
	TAT <u>CAT</u> CTGTATTATCGTTGTCTGTATGTTGATTTCTTGATGTTTCGTTAACATGTTTT
	605 acc1,
4420	IleGlnAsnPheArgValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAla
	662 ATTCAAAATTTCGGGTTTATTACAGGGACAACAAAGATCCCCTTGGAAAGGACCAGCA
	TAAGTTTAAAGCCCAAATAATGTCCTGTT <u>CT</u> AGGGGAAACCTTCTGGTCGT
	697 xho2, 698 dpn1 sau3a, 713 asul ava2,
4480	LysLeuLeuTrpLysGlyGluGlyAlaValValIleGlnAspAsnSerAspIleLysVal
	722 AAGCTTCTCTGGAAAGGTGAAGGGCAGTAGTAATA <u>CAAGATAATAGTGACATAAAAGTA</u>
	<u>TT</u> CGAAGAGACCTTCCACTTCCCCGT <u>CAT</u> TATTATGTTCTATTATCACTGTATTTCAT
	722 hind111, 723 alu1, 737 hph,
4540	ValProArgArgLysAlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAsp
	782 GTGCCAAGAAGAAAAGCAAAATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGAT
	<u>CACGGTT</u> CTTCTTTCTGTTTAGTAATCCCTAACCTTTGTCTACCGT <u>CC</u> ACTACTA
	789 mboll, 833 hph,
4600	CysValAlaSerArgGlnAspGluAsp <u>AM</u>
	842 TGTGTGGCAAGTAGACAGGATGAGGATTAGTCGACGGAATTCTTTAGTAAAACACC
	ACACACCGTT <u>CAT</u> CTGT <u>C</u> TACTCCTAAC <u>TCAG</u> CTGC <u>CT</u> AAAGAAAT <u>CATT</u> GTGG
	852 acc1, 859 fok1, 863 mn11, 871 acc1 hind11 sal1, 872 taq1
	, 878 ecor1,

FIG. 12B

REPLACEMENT SHEET

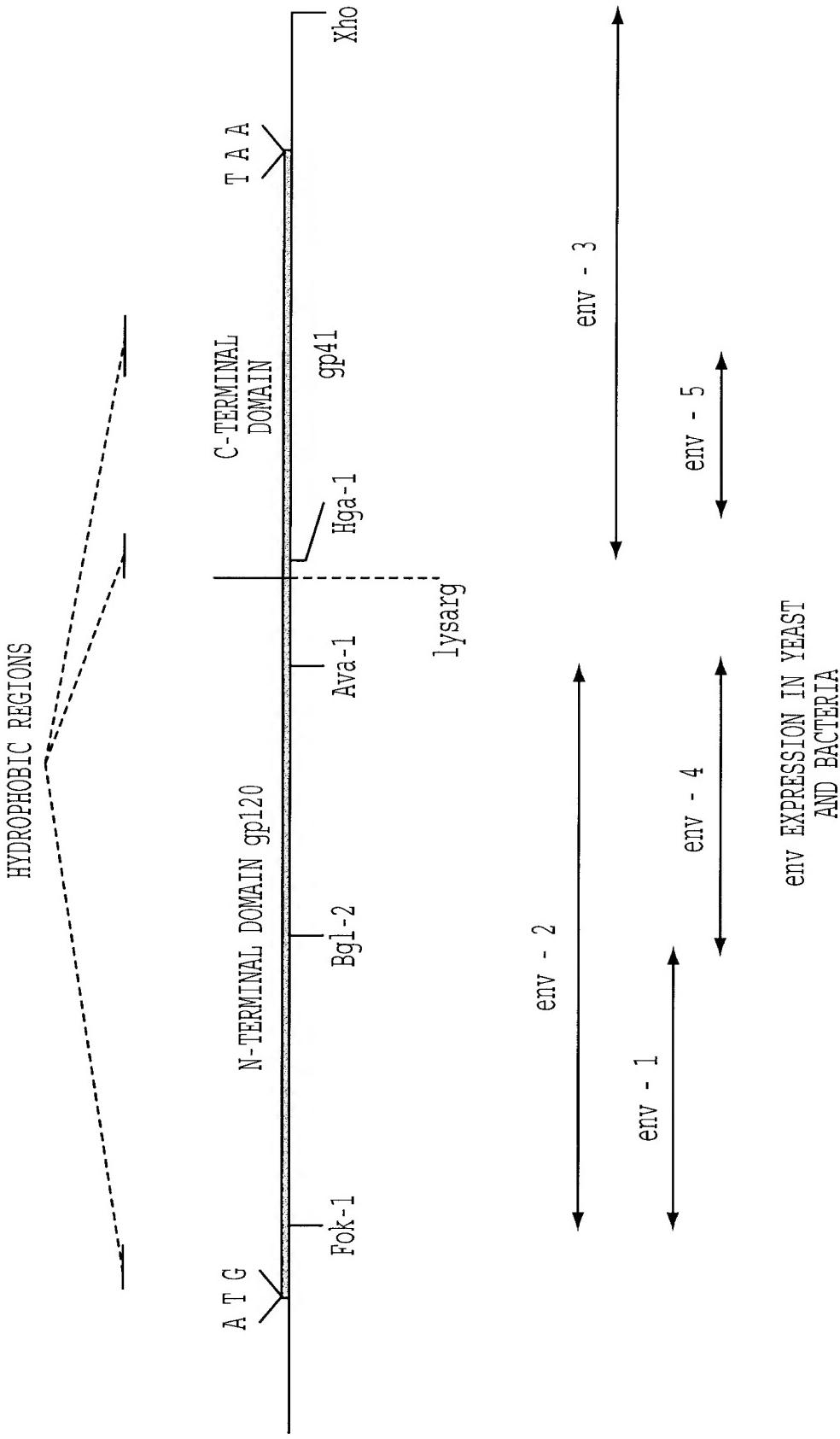


FIG. 13

REPLACEMENT SHEET

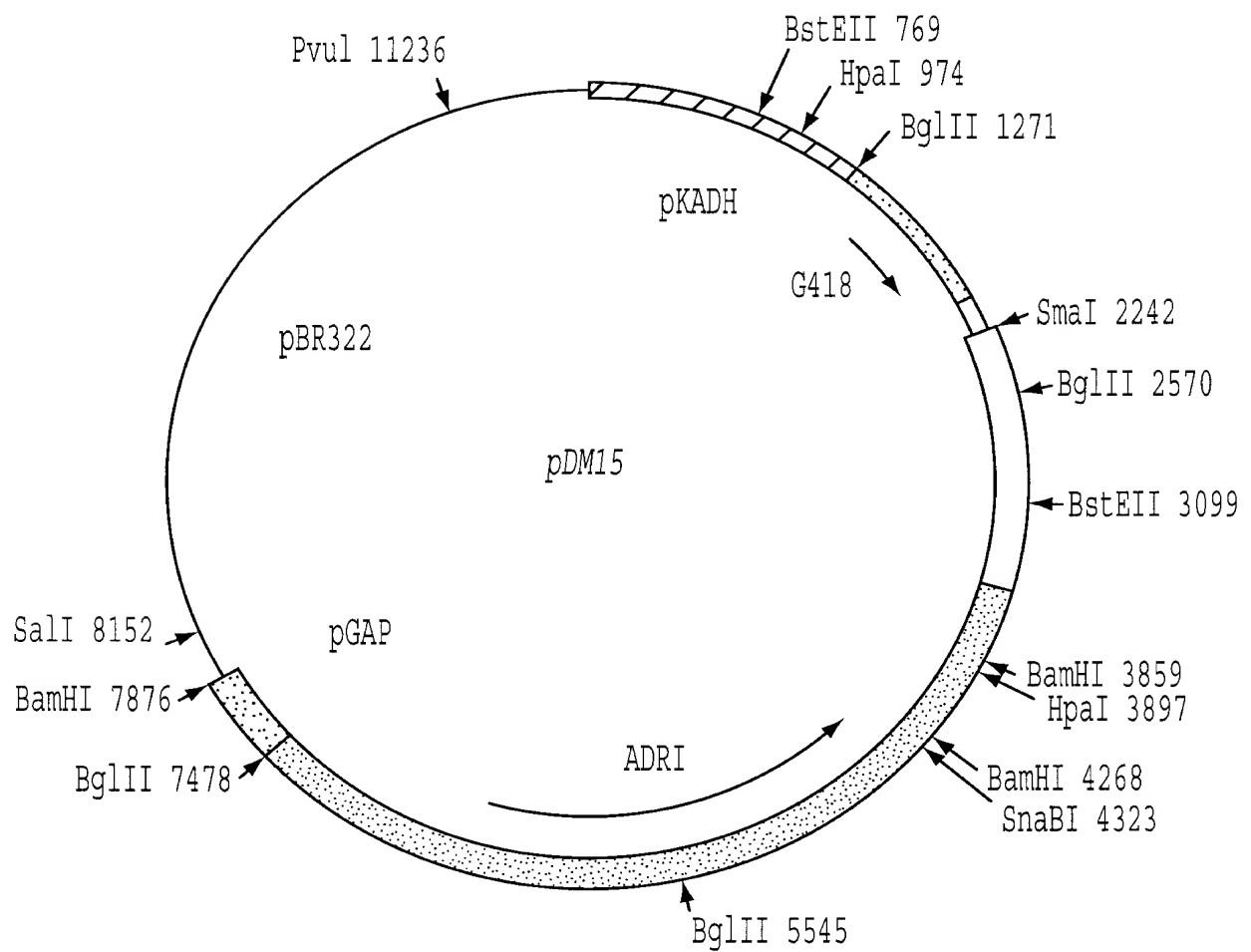


FIG. 14

REPLACEMENT SHEET

SOD

Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Glu Gly Ile Ile Asn
 1 CATGGCGACGAAGGCCGTGCGTGCCTGAAGGGCGACGGCCCAGTGCAGGGCATCATCAAT
 CGCTGCTTCCGGCACACGCACGACTTCCGCTGCCGGGTACGTCCCGTAGTAGTTA

Phe Glu Glu Lys Glu Ser Asn Gly Pro Val Lys Val Trp Gly Ser Ile Lys Gly Leu Thr
 62 TTCGAGCAGAAGGAAAGTAATGGACCACTGAAGGTGTGGGGAAAGCATTAAAGGACTGACT
 AAGCTCGTCTTCCTTCATTACCTGGTCACTTCCACACCCCTCGTAATTTCCTGACTGA

Glu Gly Leu His Gly Phe His Val His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser
 122 GAAGGCCCTGCATGGATTCCATGTTCATGAGTTGGAGATAATAACAGCAGGCTGTACCAGT
 CTTCCGGACGTACCTAAGGTACAAGTACTCAAACCTCTATTATGTCGTCCGACATGGTCA

Ala Gly Pro His Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg
 182 GCAGGGTCCTCACTTAATCCTCTATCCAGAAAACACGGTGGGCCAAAGGATGAAGAGAGG
 CGTCCAGGAGTGAAATTAGGAGATAGGTCTTGTGCCACCCGGTTCTACTTCTCTCC

His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala Asp Val Ser Ile
 242 CATGTTGGAGACTTGGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT
 GTACAACCTCTGAACCCGTTACACTGACGACTGTTCTACCACACCCGGCTACACAGATAA

Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys Ile Ile Gly Arg Thr Leu Val Val
 302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTGCATCATTGCCGCACACTGGTGGTC
 CTTCTAACAGACACTAGAGTGAGAGTCTGTGGTAACGTAGTAACCGCGTGTGACCAACAG

His Glu Lys Ala Asp Asp Leu Gly Lys Gly Asn Glu Ser Thr Lys Thr Gly Asn
 362 CATGAAAAAGCAGATGACTTGGGCAAAGGTGGAAATGAAGAAAGTACAAAGACAGGAAAC
 GTACTTTTCGTCTACTGAACCCGTTCCACCTTACTTCTTCTGTTCTGTCCTTGT

ENV 5B

Ala Gly Ser Arg Leu Ala Cys Gly Val Ile Gly Ile Ala Met Ala Ile Glu Ala Glu Gln
 422 GCTGGAAAGTCGTTGGCTTGTGGTGTAAATTGGGATGCCATGGCTATCGAAGCTAACAA
 CGACCTTCAGCAAACCGAACACACATTAAACCCTAGCGGTACCGATAGCTCGAGTTGTT

His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val
 482 CACTTGCTGCAGTTGACCGTTGGGTATCAAGCAGTGCAGGCTAGAGTTGGCTGTT
 GTGAACGACGTCAACTGGCAAACCCCATAGTTGTCACACGTCCGATCTCAAAACCGACAA

Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
 542 GAAAGATACTTGAGAGATCAACAATTGTTGGGTATCTGGGTTGTTCTGGTAAGTTGATT
 CTTTCTATGAACTCTCTAGTTGTTAACAAACCCATAGACCCCCAACAGACCATTCAACTAA

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Asp Ile Trp
 602 TGTACCACCGCTGTCCTGGAACGCTCTGGCTAACAGTCTTGGAAAGACATCTGG
 ACATGGTGGCGACAAGGGACCTTGCAGAAGAACCCAGATTGTTAGAAACCTCTGTAGACC

Asp Asn Met Thr Trp Met Gln Trp Glu Arg Glu Ile Asp Asn Tyr Thr Asn Thr Ile Tyr
 662 GACAACATGACCTGGATGCAATGGGAAAGAGAAATCGACAACACCAACACCATCTAC
 CTGTTGACTGGACCTACGTTACCCCTCTTAGCTGTTGATGTGGTTGGTAGATG

Thr Leu Leu Glu Glu Ser Gln Asn Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu
 722 ACCTTGGGAGGAATCTCAAAACCAACAAAGAAAAGAACGAAACAAGAACGAAATTGTTGGAAATTG
 TGGAAACAACCTCTTAGAGTTGGTTGTTCTTGTGTTCTAACACCTTAAC

Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp AM
 782 GACAAGTGGGCAAGCTGTGGAACTGGTCTCTATCACCAACTGGTAG
 CTGTTCACCCGTTGAACACCTTGACCAAGAGATAGTGGTTGACCATCAGCT

Translated Mol. Weight = 30414.22

FIG. 15

REPLACEMENT SHEET

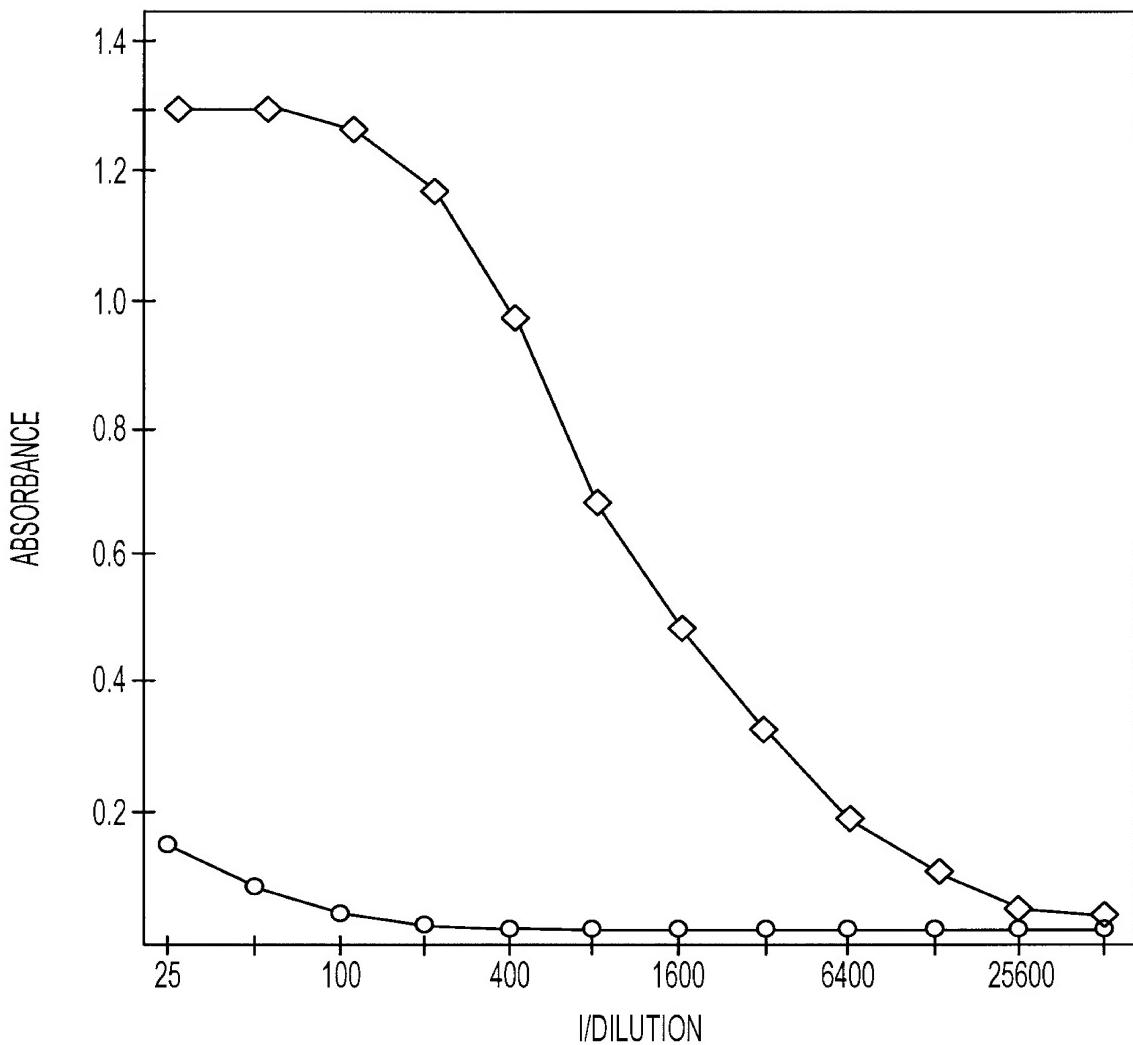


FIG. 16A

REPLACEMENT SHEET

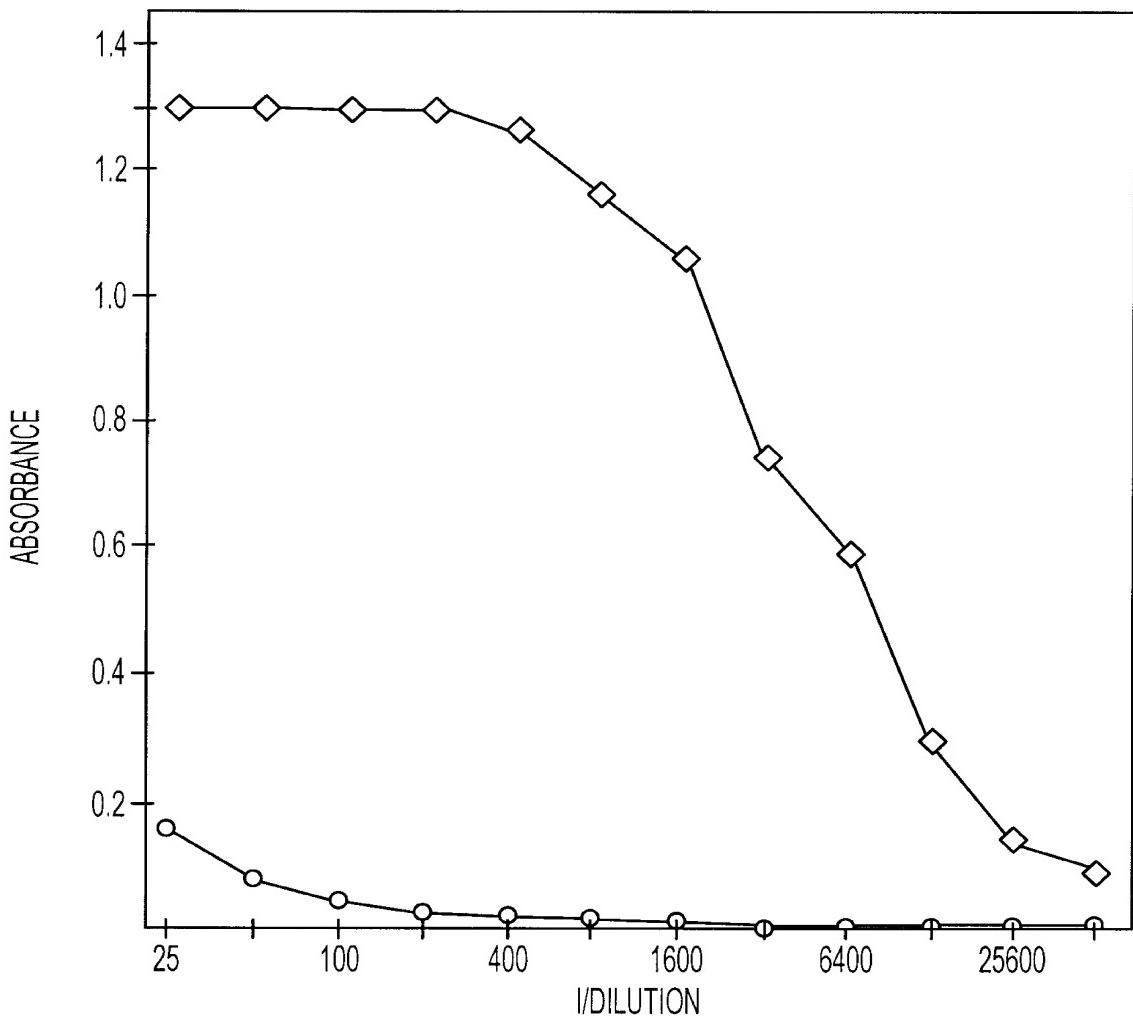


FIG. 16B

REPLACEMENT SHEET

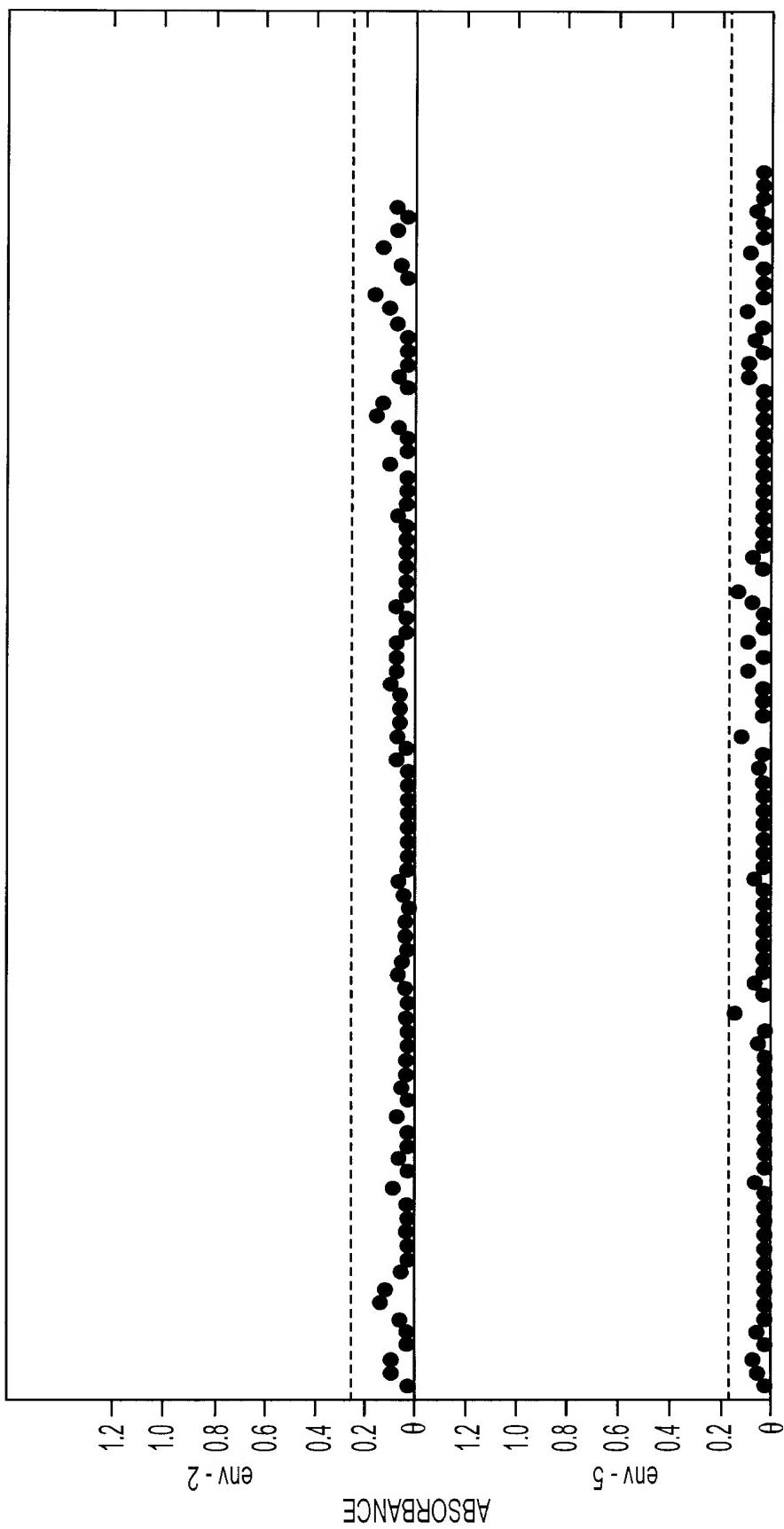


FIG. 17

REPLACEMENT SHEET

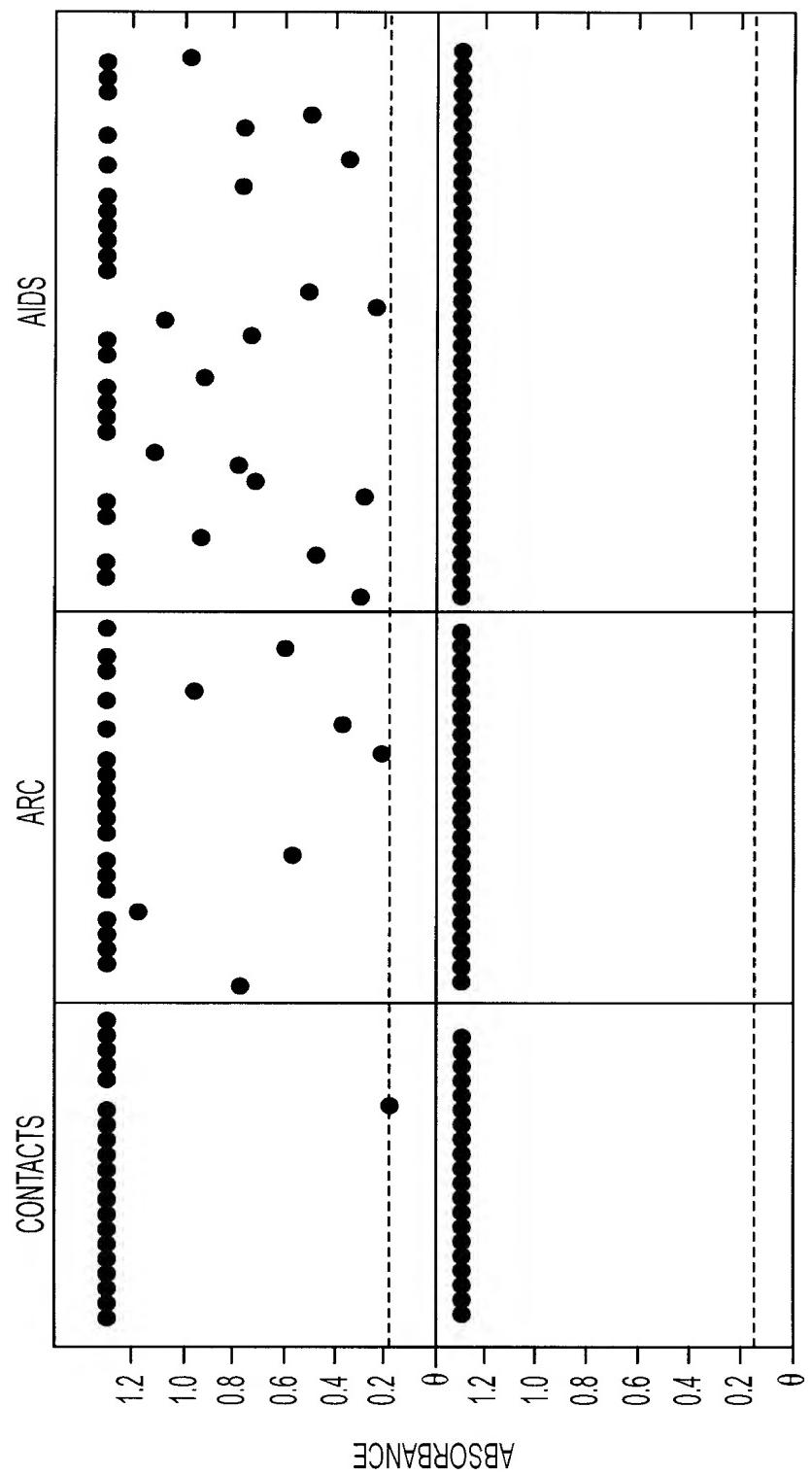


FIG. 18

REPLACEMENT SHEET

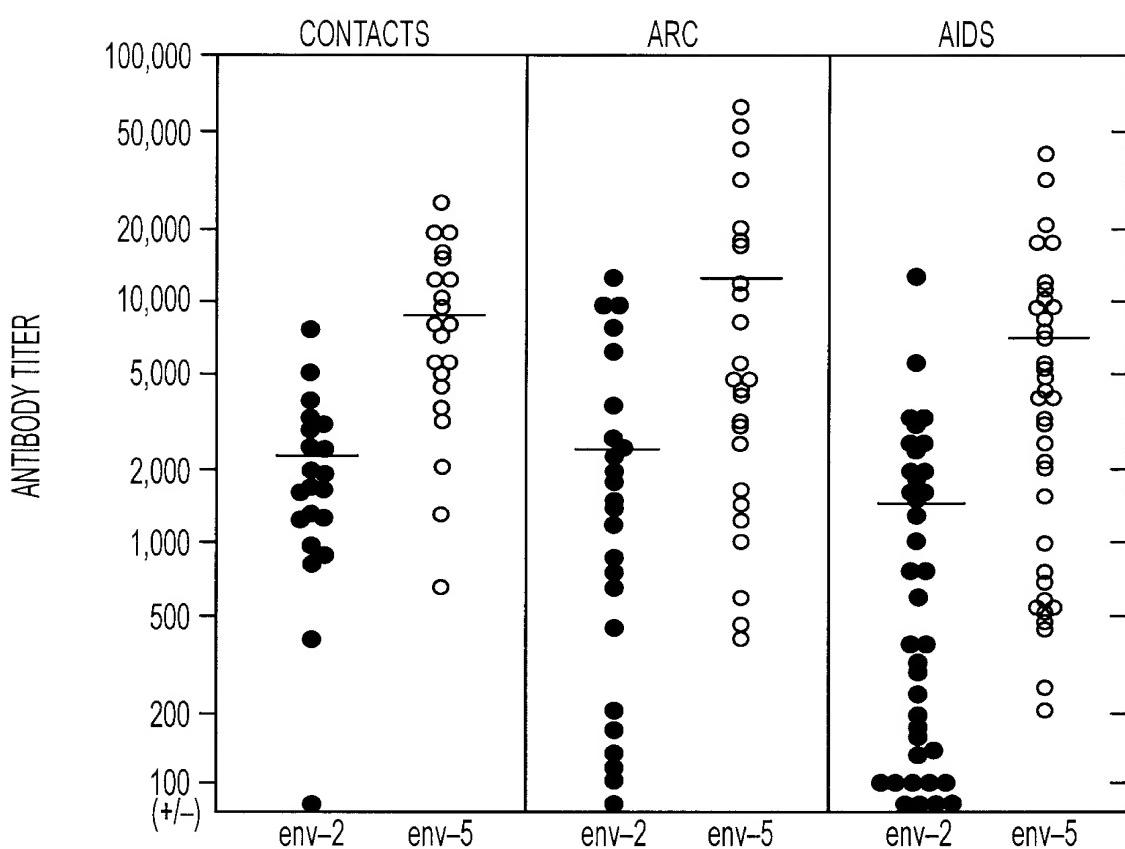


FIG. 19

REPLACEMENT SHEET

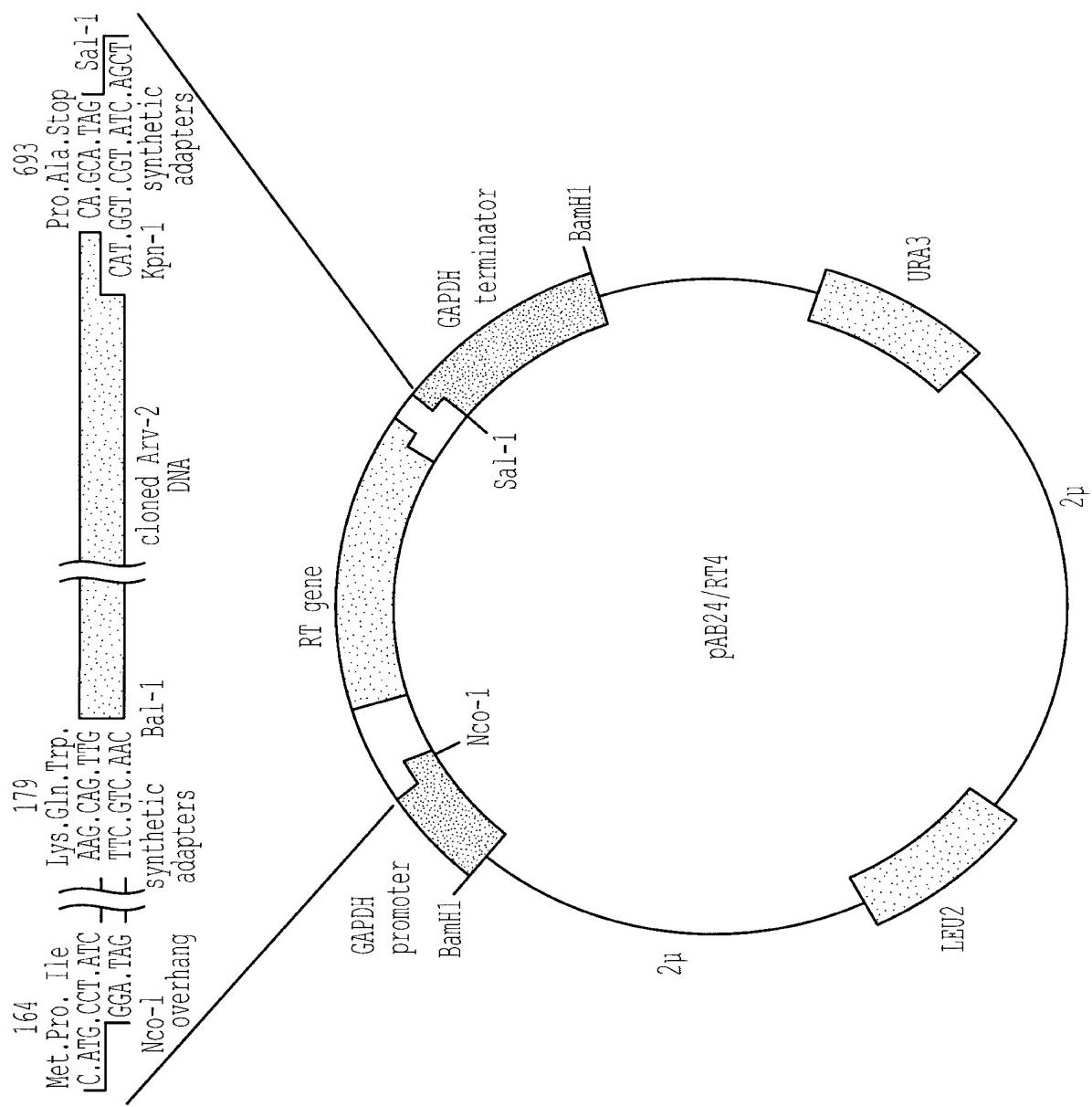


FIG. 20

REPLACEMENT SHEET

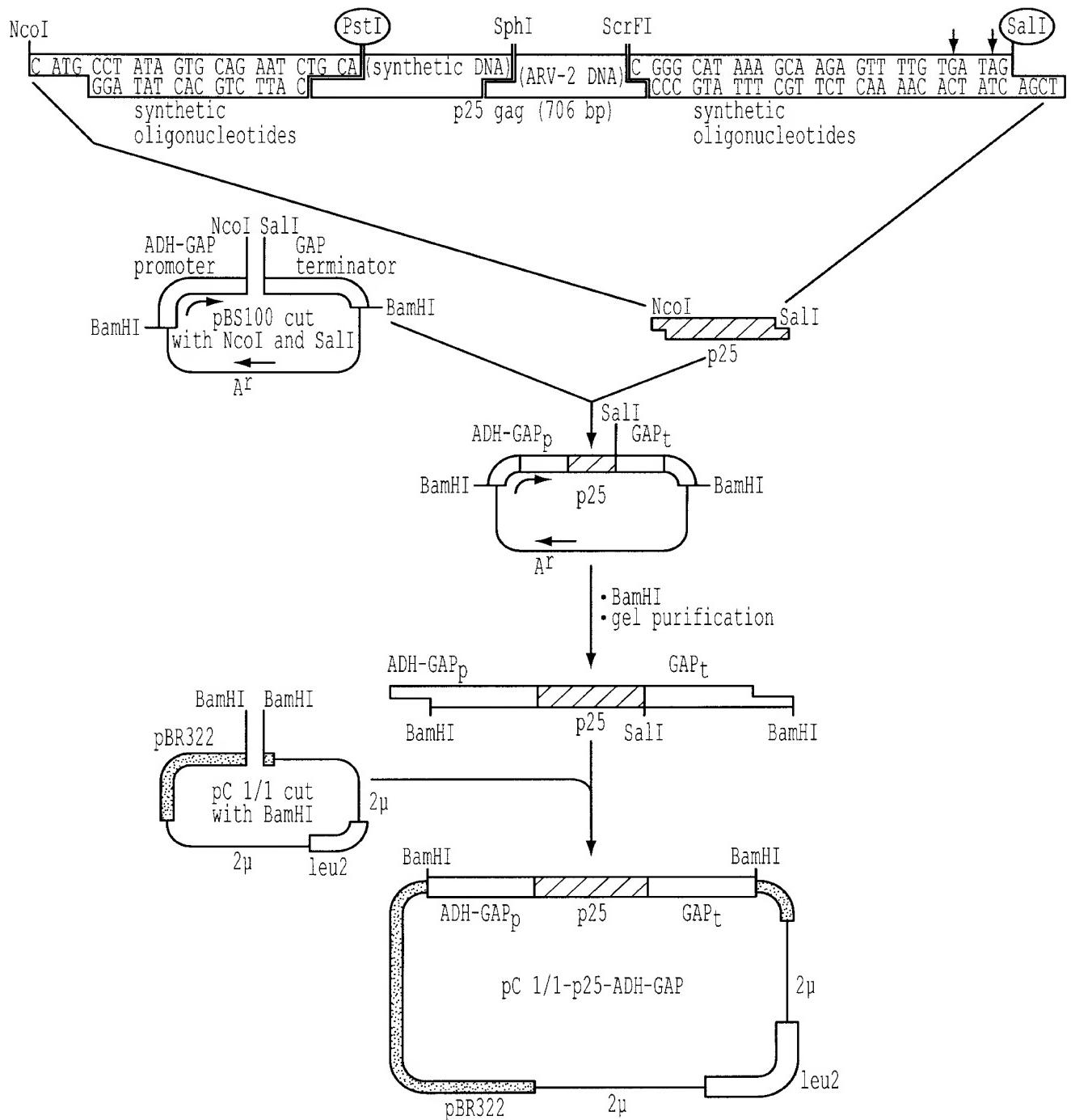


FIG. 21

REPLACEMENT SHEET

C	1	Met	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	Gln	10
		ATG	CCT	ATA	GTG	CAG	AAT	CTG	CAG	GGG	CAA	ATG	GTA	CAT	CAG	
<hr/>																
	20	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
		GCC	ATA	TCA	CCT	AGA	ACT	TTA	AAT	GCT	TGG	GTA	AAA	GTA	GTA	GAA
<hr/>																
	30	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu
		GAA	AAG	GCT	TTC	AGC	CCA	GAA	GTA	ATA	CCC	ATG	TTT	TCA	GCA	TTA
<hr/>																
	50	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr
		TCA	GAA	GGA	GCC	ACC	CCT	CAA	GAT	TTA	AAC	ACC	ATG	CTA	AAC	ACA
<hr/>																
	60	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile
		G TG	GGG	GG A	CAT	CAA	GCA	GCC	AT G	CAA	AT G	TT A	AAA	GAG	ACT	AT C
<hr/>																
	80	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala
		AAT	GAG	GAG	GCT	GCC	GAA	TGG	GAT	AGA	GTG	CAT	CCA	GTG	CAT	GCA
<hr/>																
	90	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp
		GGG	CCT	ATT	GCA	CCA	GGC	CAA	ATG	AGA	GAA	CCA	AGG	GG A	AGT	GAC
<hr/>																
<hr/>																

FIG. 22A

REPLACEMENT SHEET

Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
110
ATA GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG

Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp
120
ACA AAT AAT CCA CCT ATC CCA GTA GGA GAA ATC TAT AAA AGA TGG

Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
140
ATA ATC CTG GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC

Ser Ile Leu Asp Ile Arg Gin Gly Pro Lys Glu Pro Phe Arg Asp
150
AGC ATT CTG GAC ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAT

Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
170
TAT GTA GAC CGG TTC TAT AAA ACT CTA AGA GCC GAA CAA GCT TCA

Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn
180
CAG GAT GTA AAA AAT TGG ATG ACA GAA ACC TTG TTG GTC CAA AAT

Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
200
GCA AAC CCA GAT TGT AAG ACT ATT TTA AAA GCA TTG GGA CCA GCA

Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
210
GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG GGA GTG GGG GGA

Pro Gly His Lys Ala Arg Val Leu OP
230 232
CCC GGG CAT AAA GCA AGA GTT TTG TGA TAG

Translated Mol. Weight = 25700.75

FIG. 22B

REPLACEMENT SHEET

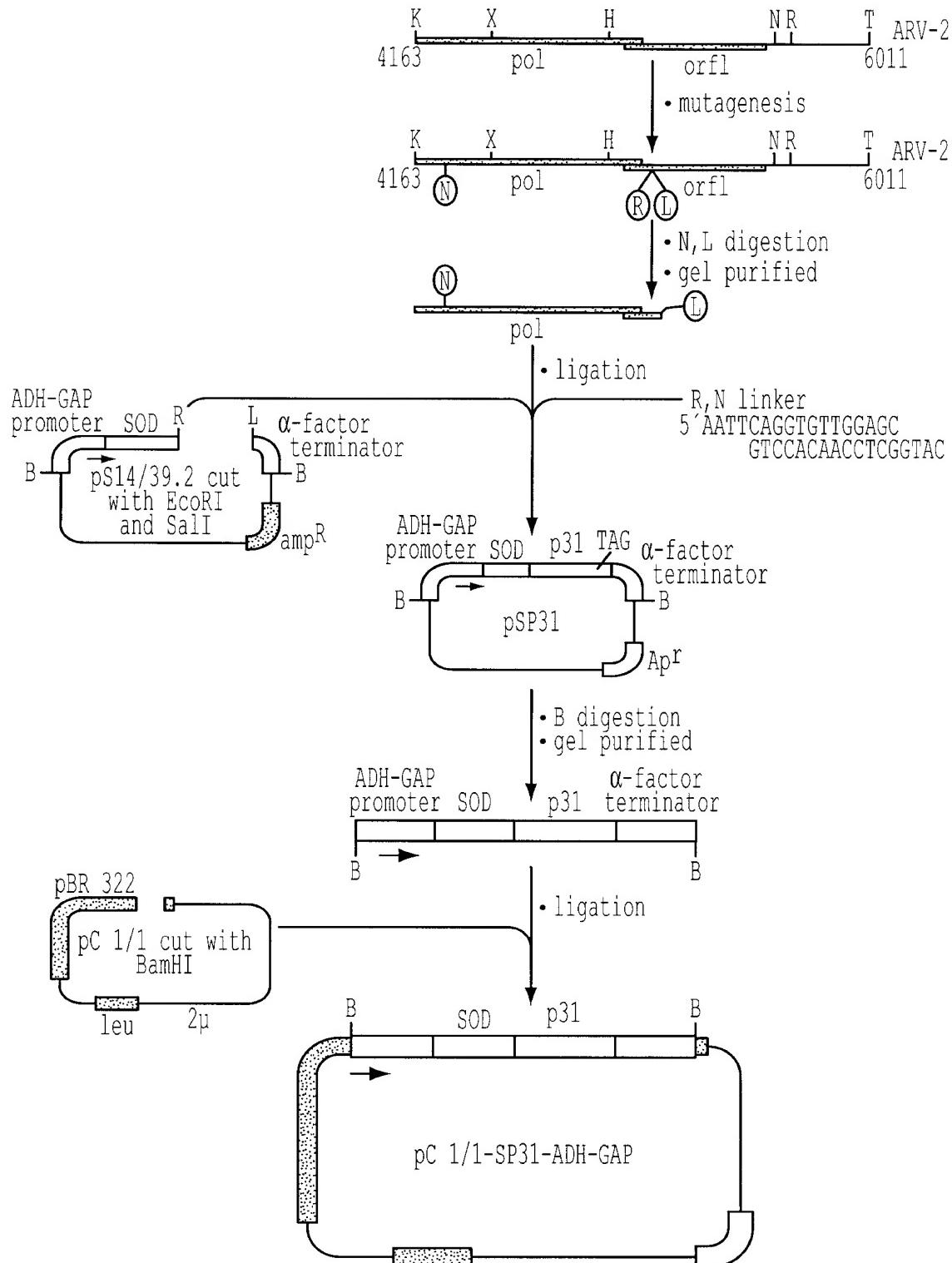


FIG. 23

REPLACEMENT SHEET

SOD-->
MetAlaThrLysAla
ATGGCTACAAAGGCT
TACCGATGTTCCGA

1383 ValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsnPheGluGlnLysGlu
GTTTGTTTGAAGGGTGACGGGCCAGTTCAAGGTATTATAACTTCGAGCAGAAGGAA
CAAACACAAAACCTCCCACGTGCCGGGTCAGTTCCATAATAATTGAAGCTCGTCTTCCTT

1443 SerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThrGluGlyLeuHisGly
AGTAATGGACCACTGAAGGTGTGGGGAAAGCATTAAAGGACTGACTGAAGGCCTGCATGGG
TCATTACCTGGTCACTTCCACACCCCTCGTAATTTCCTGACTGACTTCCGGACGTACCT

1503 PheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSerAlaGlyProHisPhe
TTCCATGTTCATGAGTTGGAGATAATACAGCAGGCTGTACCAGTGCAGGTCTCACTTT
AAGGTACAAGTACTCAAACCTCTATTATGTCGTCCGACATGGTCACGTCCAGGAGTGAAC

1563 AsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArgHisValGlyAspLeu
AATCCTCTATCCAGAAAACACGGTGGGCCAAGGATGAAGAGAGGCATGTTGGAGACTTG
TTAGGAGATAGGTCTTTGTGCCACCCGGTTCTACTTCTCTCCGTACAACCTCTGAAC

1623 GlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIleGluAspSerValIle
GGCAATGTGACTGCTGACAAGATGGTGTGCCGATGTGTCTATTGAAGATTCTGTGATC
CCGTTACACTGACGACTGTTCTACCACACCGGCTACACAGATAACTCTAAGACACTAG

1683 SerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValValHisGluLysAlaAsp
TCACTCTCAGGAGACCATTGCATCATGGCCGACACTGGTGGTCCATGAAAAAGCAGAT
AGTGAGAGTCCTCTGGTAACGTAGTAACCGGCGTGTGACCACCAGGTACTTTCTGCTA

1743 AspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsnAlaGlySerArgLeu
GACTTGGGAAAGGTGGAAATGAAGAAAGTACAAAGACAGGAAACGCTGGAAAGTCGTTG
CTGAACCCGTTCCACCTTACTTCTTATGTTCTGCTTGCACCTCAGCAAAC

linker --> p31 -->

1803 AlaCysGlyValIleGlyIleAlaGlnAsnSerGlyValGlyAlaMetAlaMetAlaSer
GCTTGTTGTAATTGGGATGCCAGAATTCAAGGTGTTGGAGCCATGCCATGGCTAGT
CGAACACACATTAACCTAGCGGGTCTTAAGTCCACAAACCTCGGTACCGGTACCGATCA

1863 AspPheAsnLeuProProValValAlaLysGluIleValAlaSerCysAspLysCysGln
GATTTAACCTGCCACCTGTAGTAGCAGGAAATAGTAGCCAGCTGTGATAATGTCAG
CTAAAATTGGACGGTGGACATCATCGTTTCTTATCATCGGTGACACTATTACAGTC

1923 LeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGlyIleTrpGlnLeuAsp
CTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGAT
GATTTCCCTTCGGTACGTACCTGTTCATCTGACATCAGGTCCCTATACCGTTGATCTA

FIG. 24A

REPLACEMENT SHEET

1983 CysThrHisLeuGluGlyLysIleIleLeuValAlaValHisValAlaSerGlyTyrIle
 TGTACACATCTAGAAGGAAAAATTATCCTGGTAGCAGTCATGTAGCCAGTGGATATATA
 ACATGTGTAGATCTTCCTTTAATAGGACCACGTCAAGTACATCGGTACCTATATAT

 2043 GluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyrPheLeuLeuLysLeu
 GAAGCAGAAGTTATTCCAGCAGAGACAGGGCAGGAAACAGCATATTTCTCTTAAAGATA
 CTTCGTCTCAATAAGTCGTCTGTCCCGTCTTGTCGTATAAAAGAGAATTTAA

 2103 AlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySerAsnPheThrSerThr
 GCAGGAAGATGGCCAGTAAAAACAATAACAGACAATGGCAGCAATTTCACCAAGTACT
 CGTCCTTCTACCGGTCACTTTGTATGTATGTCTGTACCGTCGTTAAAGTGGTCATGA

 2163 ThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsn
 ACGGTTAAGGCCGCCTGTTGGTGGCAGGGATCAAGCAGGAATTGGCATTCCCTACAAT
 TGCCAATTCCGGCGGACAACCACCCGTCCCTAGTCGTCTAAACCGTAAGGGATGTTA

 2223 ProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGln
 CCCCCAAAGTCAGGAGTAGTAGAATCTATGAATAATGAATTAAAGAAAATTAGGACAG
 GGGGTTTCAGTCCCTCATCATCTTAGATACTTATTACTTAATTCTTTAATATCCTGTC

 2283 ValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsn
 GTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCACTCCACAAT
 CATTCTCTAGTCCGACTTGTGGATTCTGTCGTATGTTACCGTCATAAGTAGGTGTTA

 2343 PheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIle
 TTTAAAAGAAAAGGGGGGATTGGGGGATACAGTGCAGGGAAAGAATAGTAGACATAATA
 AAATTCTTTCCCCCTAACCCCCCTATGTCACGTCCCTTCTTATCATCTGTATTAT

 2403 AlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArg
 GCAACAGACATACAAACTAAAGAACTACAAAAGCAAATTACAAAAATTCAAAATTTCGG
 CGTTGTCTGTATGTTGATTCTTGTGTTACCGTAAAGTTTAAGTTTAAAGTTTAAAGCC

 2463 ValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLys
 GTTATTACAGGGACAACAAAGATCCCCTTGGAAAGGACCAGCAAAGCTCTGGAAA
 CAAATAATGTCCCTGTTCTAGGGGAAACCTTCTGGTCGTTCAAGAGACCTT

 2523 GlyGluGlyAlaValValIleGlnAspAsnSerAspIleLysValValProArgArgLys
 GGTGAAGGGGCAGTAGTAATACAAGATAATAGTGACATAAAAGTAGTGCCAGAAGAAAA
 CCACTTCCCCGTACATTATGTTCTATTACTGTATTTCATCACGGTTCTTCTT

 2583 AlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArg
 GCAAAAATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGGCAAGTAGA
 CGTTTTAGTAATCCCTAACCTTTGTCTACCGTCACACTAACACACCGTTCATCT

 2643 GlnAspGluAspAM
 CAGGATGAGGATTAG
 GTCCTACTCCTAAC

FIG. 24B

REPLACEMENT SHEET

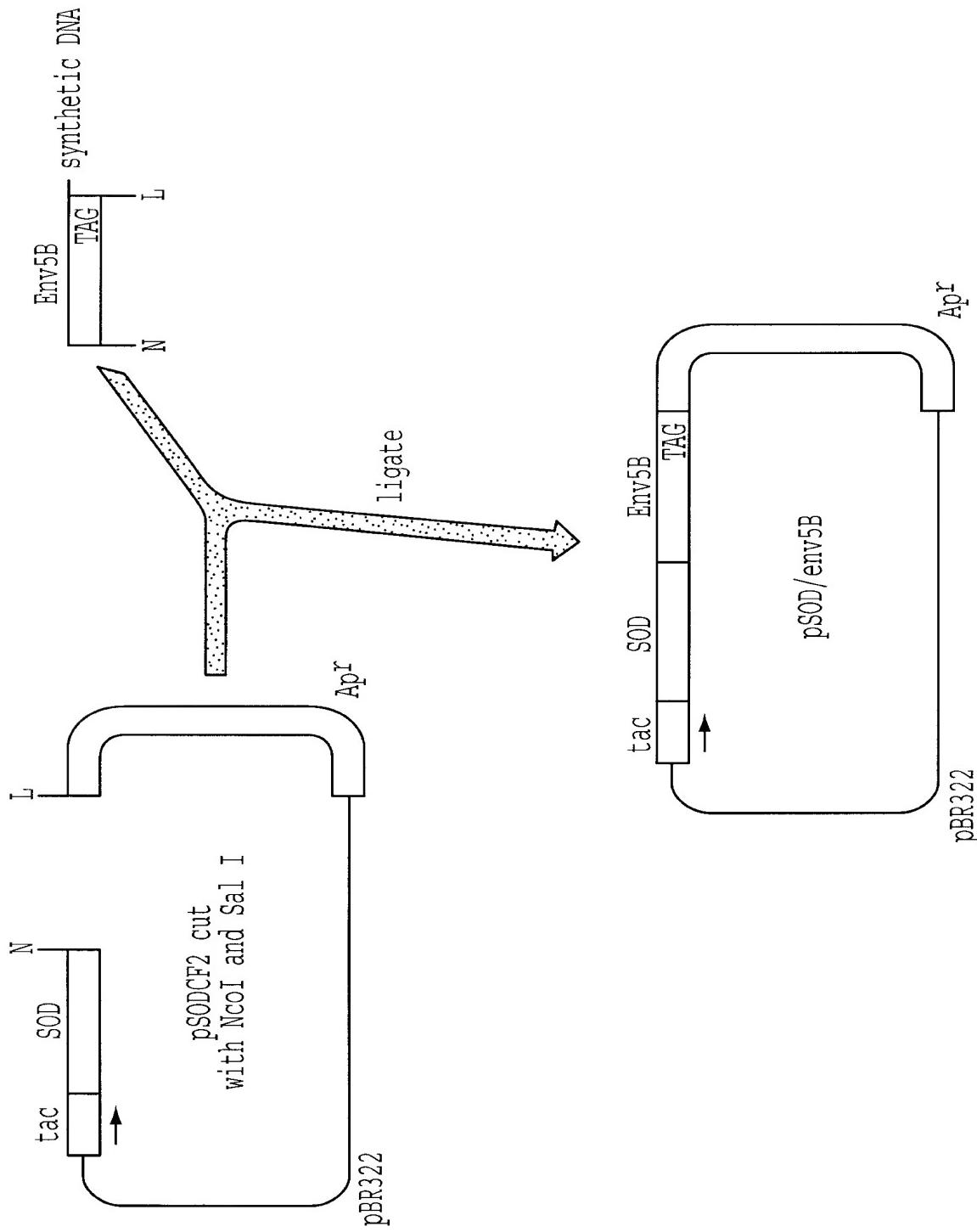


FIG. 25

REPLACEMENT SHEET

Sequence of SOD/env-4

SOD -->

MetAlaThrLysAlaValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsn
 1 CATGGCGACGAAGGCCGTGCGTGCCTGAAGGGCGACGGCCAGTGCAGGGCATCATCAAT
 CGCTGCTTCGGCACACGCACGACTTCCGCTGCCGGTCACGTCCCGTAGTAGTTA
 PheGluGlnLysGluSerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThr
 62 TTCGAGCAGAAGGAAAGTAATGGACCAGTGAAGGTGTGGGAAGCATTAAAGGACTGACT
 AAGCTCGTCTCCTTCAATTACCTGGTCACCTCCACACCCCTCGTAATTCTGACTGA
 GluGlyLeuHisGlyPheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSer
 122 GAAGGCCTGCATGGATTCCATGTTCATGAGTTGGAGATAATACAGCAGGCTGTACCAAGT
 CTTCCGGACGTACCTAACAGTACTCAAACCTCTATTATGTCGTCCGACATGGTCA
 AlaGlyProHisPheAsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArg
 182 GCAGGTCCTCACTTAATCCTCTATCCAGAAAACACGGTGGGCCAAAGGATGAAGAGAGG
 CGTCCAGGAGTGAAATTAGGAGATAGGTCTTGTGCCACCCGGTTCTACTTCTCTCC
 HisValGlyAspLeuGlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIle
 242 CATGTTGGAGACTTGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT
 GTACAACCTCTGAACCGTTACACTGACGACTGTTCTACCACACCGGCTACACAGATAA
 GluAspSerValIleSerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValVal
 302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTCGCATCATTGGCCGCACACTGGTGGTC
 CTTCTAACAGACACTAGAGTGAGAGTCCTCTGGTAACGTAGTAACCGGGGTGACCAACAG
 HisGluLysAlaAspAspLeuGlyIlysGlyAsnGluGluSerThrLysThrGlyAsn
 362 CATGAAAAAGCAGATGACTTGGCAAAAGGTGAAATGAAGAAAGTACAAAGACAGGAAAC
 GTACTTTTCGTCTACTGAACCGTTCCACCTTACTTCTTCTATGTTCTGTCCTTG

Env4 -->

AlaGlySerArgLeuAlaCysGlyValIleGlyIleAlaMetGluValValIleArgSer
 422 GCTGGAAGTCGTTGGCTTGTGGTGTAAATTGGGATGCCATGGAGGTAGTAATTAGATCT
 CGACCTTCAGCAAACCGAACACCATTAACCTAGCGGTACCTCCATCTTACAGATAATCTAGA
 ASPAsnPheThrAsnAsnAlaLysThrIleIleValGlnLeuAsnGluSerValAlaIle
 482 GACAATTTACGAACAATGCTAAACCATAATAGTACAGCTGAATGAATCTGTAGCAATT
 CTGTTAAAGTGTGTTACGATTTGGTATTATCATGTCGACTTACTAGACATCGTTAA
 AsnCysThrArgProAsnAsnAsnThrArgLysSerIleTyrIleGlyProGlyArgAla
 542 AACTGTACAAGACCCAACAACAATACAAGAAAAAGTATCTATATAGGACCAGGGAGAGCA
 TTGACATGTTCTGGGTTGTTATGTTCTTTCTAGATATATCCTGGTCCCTCGT

FIG. 26A

REPLACEMENT SHEET

602 PheHisThrThrGlyArgIleIleGlyAspIleArgLysAlaHisCysAsnIleSerArg
TTTCATAACAACAGGAAGAATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGA
AAAGTATGTTGTCCTTATTATCCTCTATATTCTTCGTGTAACATTGTAATCATCT

662 AlaGlnTrpAsnAsnThrLeuGluGlnIleValLysLysLeuArgGluGlnPheGlyAsn
GCACAATGGAATAAACACTTTAGAACAGATAGTTAAAAAAATTAAAGAGAACAGTTGGGAAT
CGTGTACCTTATTGTGAAATCTGTCTATCAATTTTAATTCTCTGTCAAACACCCTTA

722 AsnLysThrIleValPheAsnGlnSerSerGlyGlyAspProGluIleValMetHisSer
AATAAAAACAATAGTCTTAATCAATCCTCAGGAGGGGACCCAGAAAATTGTAATGCACAGT
TTATTTGTTATCAGAAATTAGTTAGGAGTCCTCCCCCTGGGTCTTAACATTACGTGTCA

782 PheAsnCysArgGlyGluPhePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrp
TTTAATTGTAGAGGGGAATTTTCTACTGTAATACAACACAACACTGTTAATAATACATGG
AAATTAAACATCTCCCTTAAAGATGACATTATGTTGTTGACAATTATTATGTAC

842 ArgLeuAsnHisThrGluGlyThrLysGlyAsnAspThrIleIleLeuProCysArgIle
AGGTTAAATCACACTGAAGGAACTAAAGGAAATGACACAATCATACTCCCATGTAGAATA
TCCAATTAGTGTGACTTCCTGATTTCTTACTGTGTTAGTATGAGGGTACATCTT

902 LysGlnIleIleAsnMetTrpGlnGluValGlyLysAlaMetTyrAlaProProIleGly
AAACAAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCATTGGA
TTTGTAAATATTGTACACCGTCCTCATCCTTCTGTTACATACGGGGAGGGTAACCT

962 GlyGlnIleSerCysSerSerAsnIleThrGlyLeuLeuLeuThrArgAspGlyGlyThr
GGACAAAATTAGTTGTTCATCAAATATTACAGGGCTGCTATTAAACAAGAGATGGTGGTACA
CCTGTTAATCAACAAGTAGTTATAATGTCCCAGCATAATTGTTCTACCAACCATGT

1022 AsnValThrAsnAspThrGluValPheArgProGlyGlyAspMetArgAspAsnTrp
AATGTAACAAATGACACCGAGGTCTCAGACCTGGAGGAGGAGATATGAGGGACAATTGG
TTACATTGATTACTGTGGCTCCAGAACGTTCTCTATAACTCCCTGTTAAC

1082 ArgSerGluLeuTyrLysTyrLysValIleLysIleGluProLeuGlyIleAlaProThr
AGAAGTGAATTATATAAAATATAAGTAATAAAAATTGAAACCTAGGAATAGCACCCACC
TCTTCACTTAATATATTATATTCAATTAACTTGTGTAATCCTTATCGTGGTGG

1142 LysAlaLysArgArgValValGlnArgGluLysArgOP OP
AAGGCCAAAGAGAAGAGTGGTGCAGAGAGAAAAAGATGATGAAGCTTG
TTCCGTTCTCTCACCACTGTCTCTTTTACTACTTCGAACAGCT

FIG. 26B

REPLACEMENT SHEET

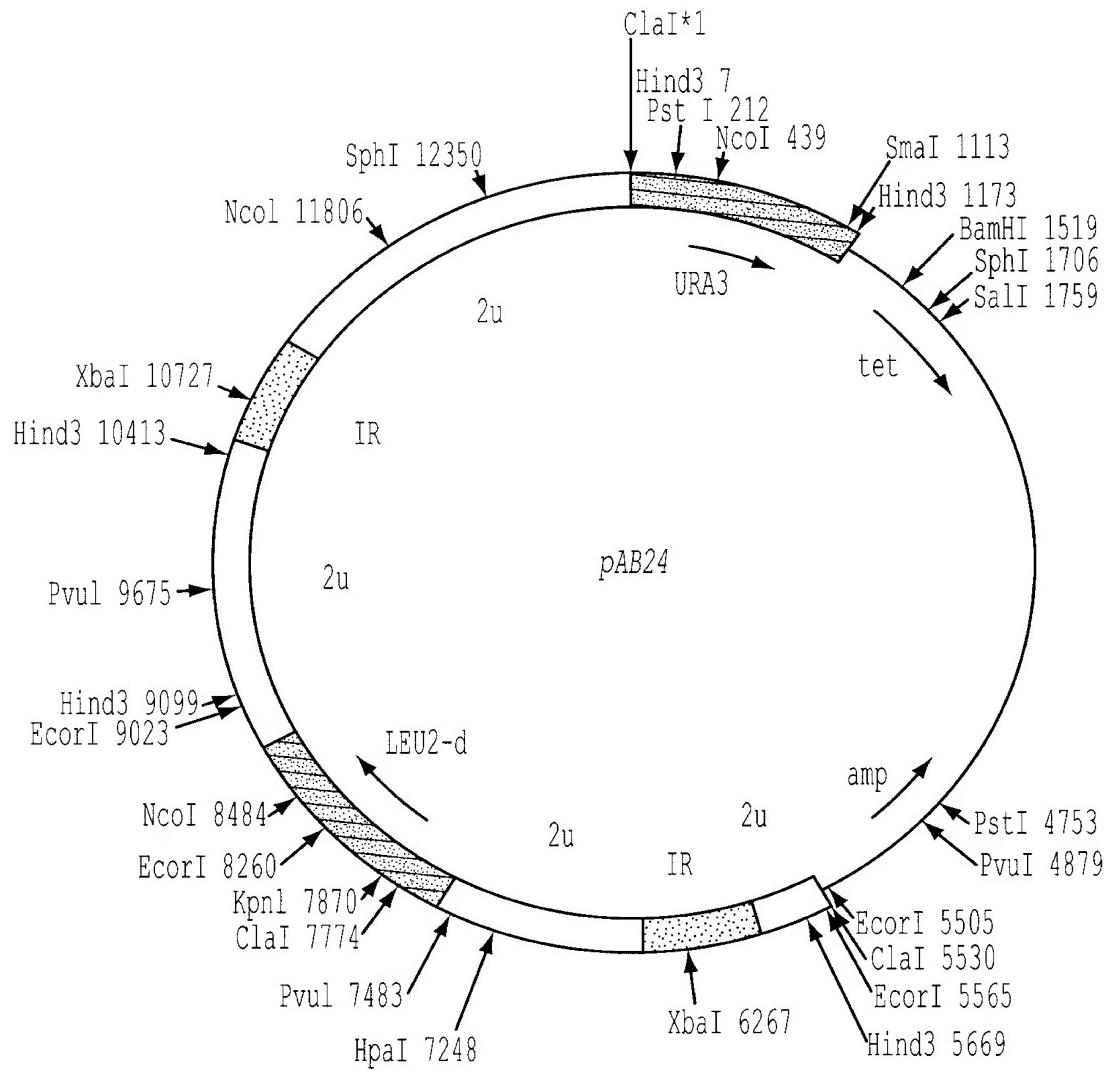


FIG. 27

REPLACEMENT SHEET

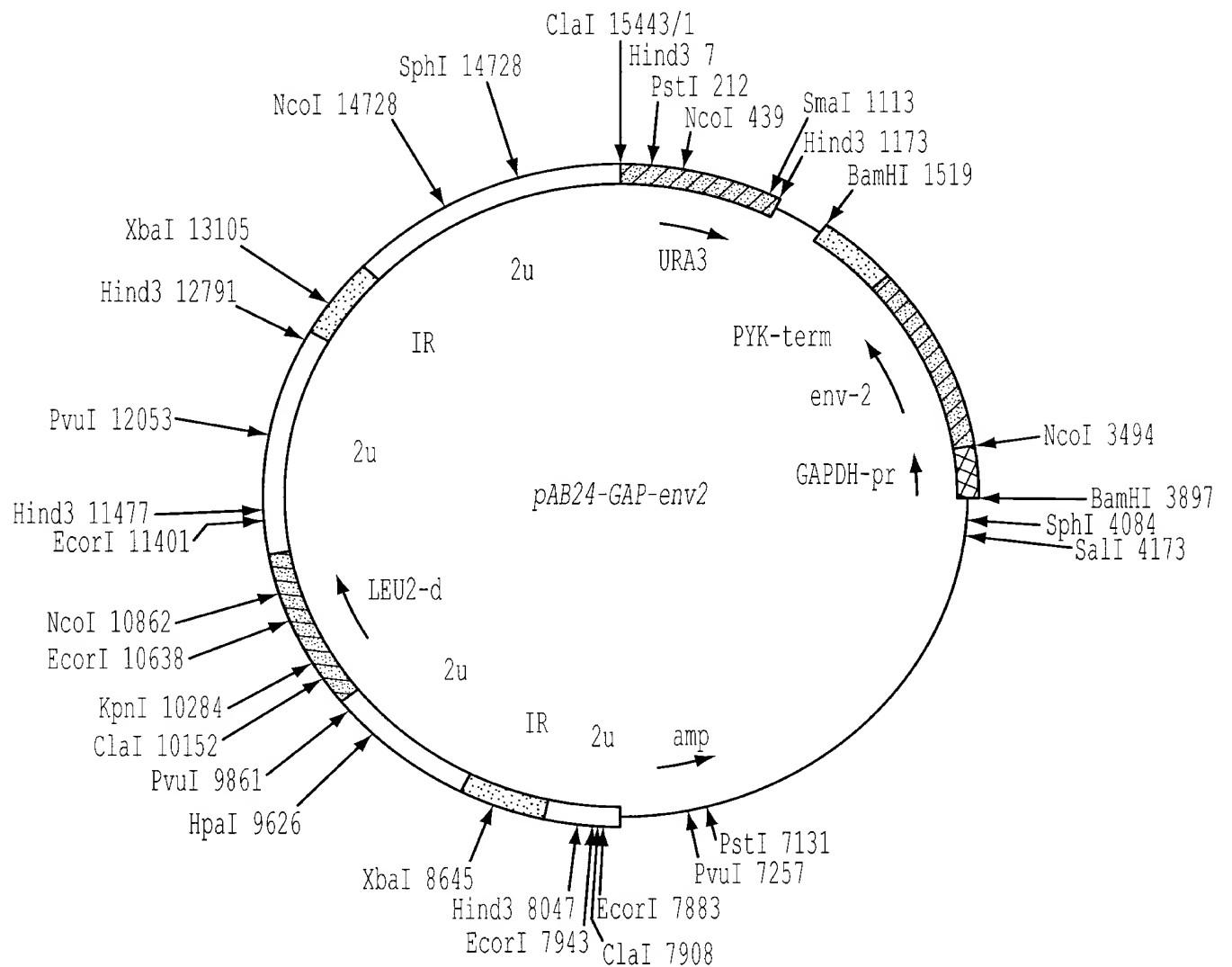


FIG. 28

REPLACEMENT SHEET

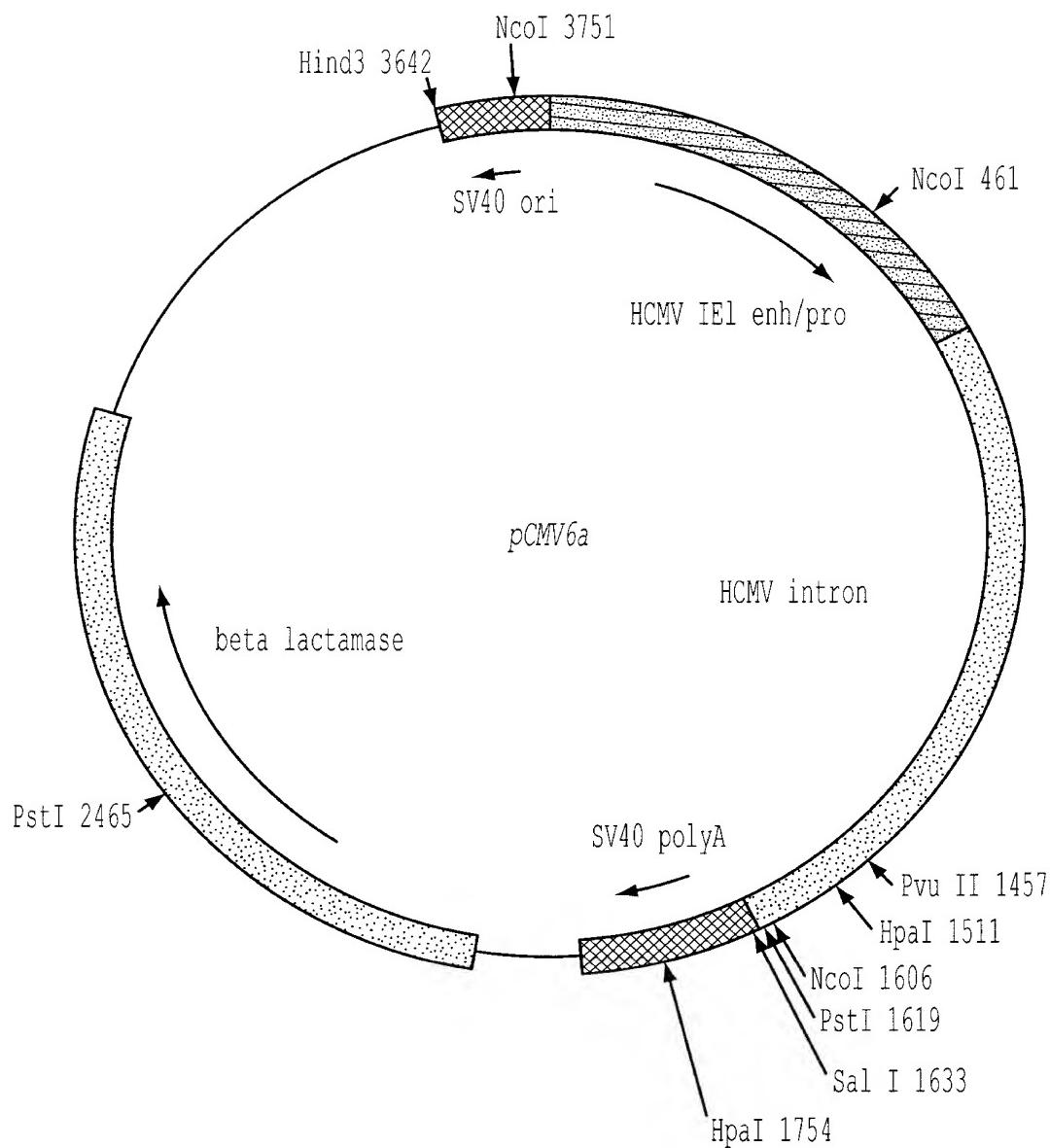


FIG. 29

REPLACEMENT SHEET

A	B	C	D	E	F
					— 200,000
					— 92,500
					— 68,000
					— 43,000
					— 25,700
					— 18,400
					— 12,300

FIG. 30

REPLACEMENT SHEET

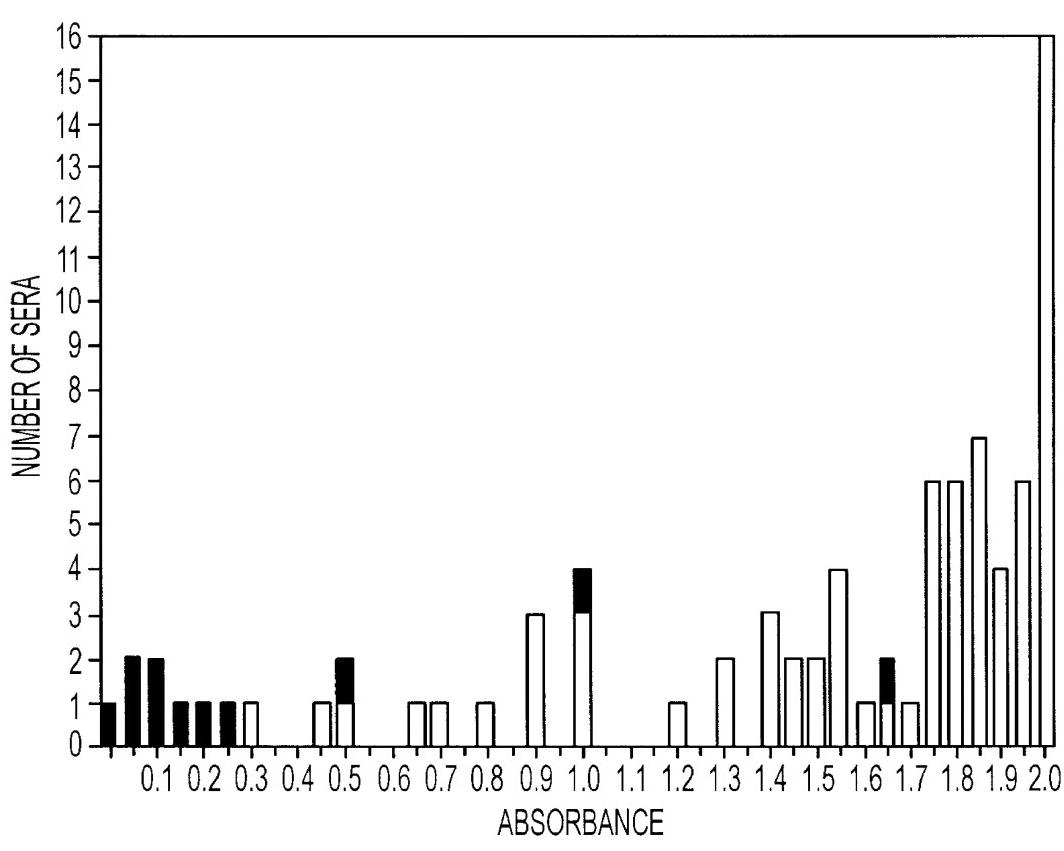
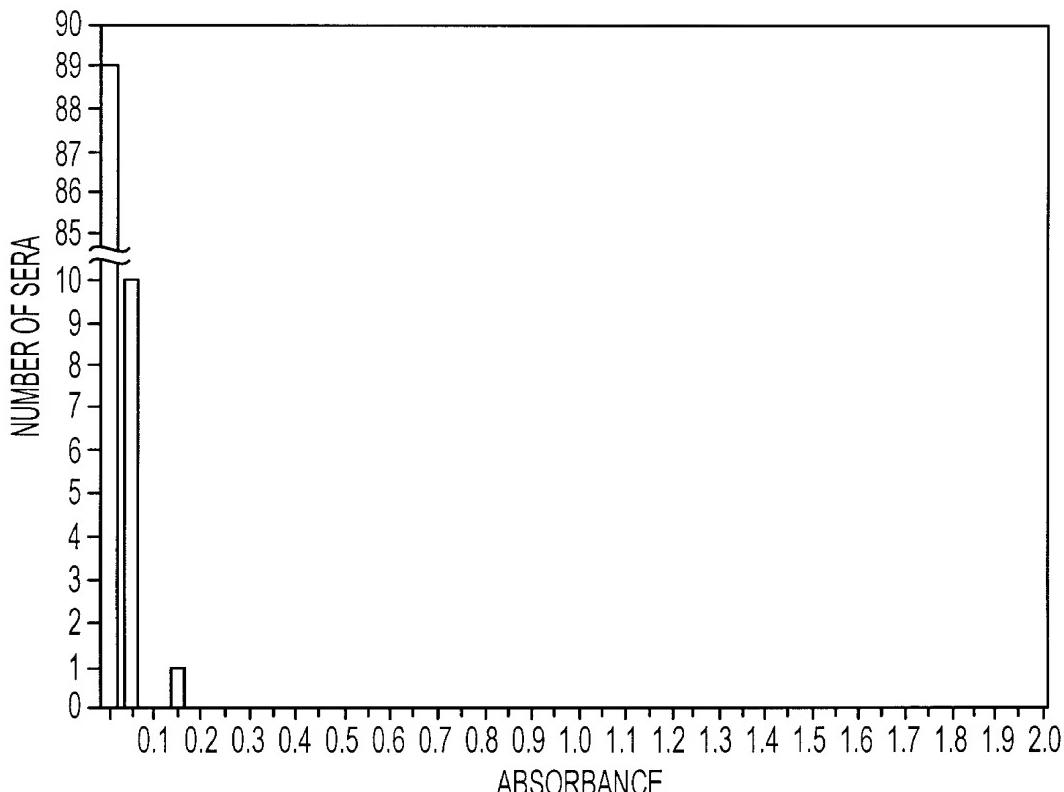


FIG. 31B